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FIGURE 1

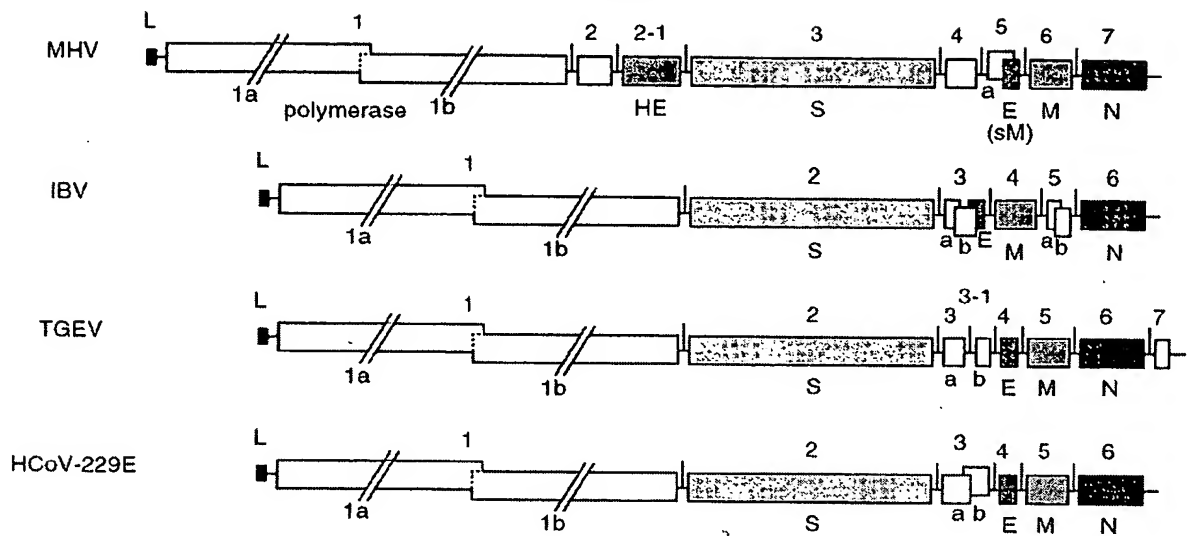


FIGURE 2

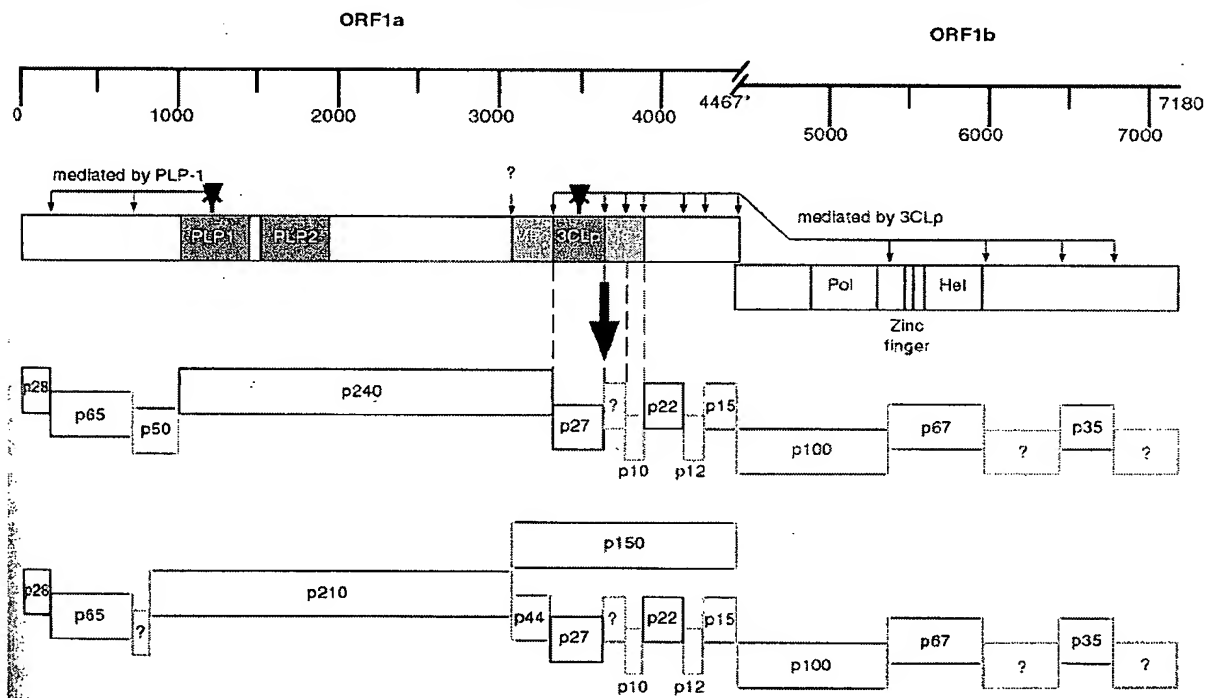


FIGURE 3**FIGURE 3A**

		Section 1					
		(1)	1	10	20	30	43
Avian infectious bronchitis N	BCV N	(1)	ATGTC	TTTTACTC	GTGGT - AAGCAAT - -	CCAGTAGTAGAGCGT	
	MHV N	(1)	ATGTC	TTTTGTTT	CGTGGGCAAGAAAAATGCCGGTGGCAGAAGCT		
		(1)	-----				
	Consensus	(1)	ATGTC	TTTT	TCCTGG	AAG AA	CC GT G AGA T
		Section 2					
		(44)	44	50	60	70	86
Avian infectious bronchitis N	BCV N	(41)	CCTTT	GGAAATCGTT	CTGGTAATGGCA	TCCTTAAG - - - - -	
	MHV N	(44)	CCTCT	GTAACCGCGCT	GGTAATGGAAATCCTCAAGAAGACCAC		
		(1)	-----				
	Consensus	(44)	CCT	TG AAA CG	CTGGTAATGG	ATCCT AAG	
		Section 3					
		(87)	87	100	110	129	
Avian infectious bronchitis N	BCV N	(76)	- TGGGC	CGATCAGT	CCGACCAATCTAGAAATGTT	CAAAACCAAG	
	MHV N	(87)	TTGGG	CTGACCAAAACCGAGCGTGGACCAATAATCAAAATAGA			
		(1)	-----ATGGCGAGCGGTAAAGCAGCTGGAAAGTCAGA				
	Consensus	(87)	TGGGC	GA CA	CCGAGCG T AAGAAAT	TCAAA CAGA	
		Section 4					
		(130)	130	140	150	160	172
Avian infectious bronchitis N	BCV N	(118)	GCTAG	AAGAGCTCAACCC	AAGCAAACTGGTACTTCTCAGCTAC		
	MHV N	(130)	GGCAG	AAGGAATCAGCCAAAGCAGACTGCAACTACTCAAC - - C			
		(33)	CTCCCC	CGCGCAATC - - ATCAAACTAGGAGGACCAAAA - - C			
	Consensus	(130)	GGCAG	AAG GCTCA CC AAGCAAACTGC ACTACTCAAC C			
		Section 5					
		(173)	173	180	190	200	215
Avian infectious bronchitis N	BCV N	(161)	CATCAGGAGGGAA	TGTTGTAAGCCTACTAT - TCTTGGTTCTCTG			
	MHV N	(171)	CAACTCC - GGGAGTGTGGTTT	CGGCATTAC - TCCTGGTTTTCGTG			
		(71)	CACCAAA - GGTAGG	TCATCTGGAAATGCATCTTGGTTTCAAG			
	Consensus	(173)	CA CA	GGGAGTGT GT CCC A TAC TCTTGGTTTTCTG			
		Section 6					
		(216)	216	230	240	258	
Avian infectious bronchitis N	BCV N	(203)	GAATTA - - - CTCAG	TTTCAAAAAGGAAAGGAGTTTGAATTTGG			
	MHV N	(212)	GCATTA - - - CCCAG	TTTCAAAAAGGAAAGGAGTTTCAAGTTTGC			
		(113)	CCATAAAGGC	CAAGAACTAAATGCACCTGCACCTAAGTTTG -			
	Consensus	(216)	GCATTA	CCCAGTT CAAAA GGAAAGGAGTTT AGTTTGC			
		Section 7					
		(259)	259	270	280	290	301
Avian infectious bronchitis N	BCV N	(243)	AGAGGGACAAGGTGTGCCTATTG	GCACCAGGAGTCCCAGCTACT			
	MHV N	(252)	AGAAAGCAAGGAGTGCCTATTGCCAATGGAATCCCGCCTTCA				
		(155)	- - AAGGTAGTGGT	CTTCTTGATAATGAAAATCTTAAAAATAGC			
	Consensus	(259)	AGAAGGACAAGGTGTGCCTATTGC	AAGGA TCCCAGCTAC			

FIGURE 3A (contd.)

Section 8					
	(302)	302	310	320	330 344
BCV N	(286)	GAAGCTAAGGGGTACTGGTACAGACACAACAGAGGTTCTTTTA			
MHV N	(295)	GAGCAAAAGGGATATTGGTATAGACACAACCGCCGTTCTTTTA			
Avian infectious bronchitis N	(196)	CAGCAGCACGGGTACTGGAGGCGCCAAGCCAG - - - - - GTTTA			
Consensus	(302)	GAGCA AAGGGGTACTGGTA AGACACAACAG CGTTCTTTTA			
Section 9					
	(345)	345	350	360	370 387
BCV N	(329)	AAACAGCCGATGGCA - ACCAGCGTCAACTGCTGCCACGATGGT			
MHV N	(338)	AAACACCTGATGGGC - AGCAGAAAGCAATTACTGCCCAGATGGT			
Avian infectious bronchitis N	(233)	AGCCAGGTAAGGCGGAAGAAAACCAAGTCCCTGATGCG - TGGT			
Consensus	(345)	AAACAGCTGATGGC A CAGAA CAATT CTGCC CGATGGT			
Section 10					
	(388)	388	400	410	420 430
BCV N	(371)	ATTTTACTATGTTGGAACAGGACCGCATGCCAAGAGCCAGTA			
MHV N	(380)	ATTTTACTATGTTGGAACAGGACCGCATGCCAAGAGCCAGTA			
Avian infectious bronchitis N	(275)	ATTTCTATTACACTGGAACAGGACCGCCCTGACCTGAATTG			
Consensus	(388)	ATTTTACTATCTTGGAAACAGGACC CATGCTGAAG CAATTA			
Section 11					
	(431)	431	440	450	460 473
BCV N	(414)	TGGCACCGATATTGACGGAGTCTCTGCGGTGCGTAGTAACAG			
MHV N	(423)	TGGAGACAGCAATTGAAGGTGCTCTCTGGGTGCGTAACAGCCAA			
Avian infectious bronchitis N	(318)	GGGTGATTCTCAAGATGGTATAGTGTGGGTGCGTGAAGGGT			
Consensus	(431)	TGG GAC TATTGA GGTGTCTTCTGGGTTGCTA TAACCA			
Section 12					
	(474)	474	480	490	500 516
BCV N	(457)	GCTGATGTCAATAACCCGGCTGACATTCTCGATCGGGACCCAA			
MHV N	(466)	GCGGACACCAATAACCCGCTCTGATATTGTGGAAGGGAACCAA			
Avian infectious bronchitis N	(361)	GCTGATGTGAAATCTAGATCCAAACAGGGTACTAGAGATCCTG			
Consensus	(474)	GCTGATGTCAATAACCCG TCTGACATTGTGATAGGGACCCAA			
Section 13					
	(517)	517	530	540	559
BCV N	(500)	GTAGCGATGAGGCTATTCCGACTA - GGTTCGCGCTGGCACGG			
MHV N	(509)	GCAATCATGAGGCTATTCCCTACTA - GGTTCGCGCGCGCACGG			
Avian infectious bronchitis N	(404)	ATAAGTTTGAT - CAATACCCACTACGGTTTTCAGATGG - - - - -			
Consensus	(517)	GTAG ATGAGGCTATTCC ACTA GGTTC CGCCTGGCACGG			
Section 14					
	(560)	560	570	580	590 602
BCV N	(542)	TACTCCCTCAGGCTTACTATATTGAAGGCTCAGGAAGGTCCTGC			
MHV N	(551)	TATTGCCCTCAGGCTTTTATGTTGAAGGCTCTGGAAGGTCCTGC			
Avian infectious bronchitis N	(441)	- AGGACCTGATGGTAATT - - - - - TCCGTTGGGACTTC			
Consensus	(560)	TA T CCTCAGGCTTATTAT TTGAAGGCTC GGAAGGTCCTGC			

FIGURE 3A (contd.)

						Section 15
	(603)	603	610	620	630	645
BCV N	(585)	TCCTAATTCCAGATCTACTTCACGCGCA--TCCAGTAGAGCG				
MHV N	(594)	ACCTGCTAGCCGATCTGTTTCGCGGTCACAATCCCGTGG-GCC				
Avian infectious bronchitis N	(472)	AT-TCCTCTGAGTCGTGGTAGGAGTGGGAAGATCAACCGCAGCA				
Consensus	(603)	ACCT	CT	CAGATCTGGTTCGCG	GCA	ATCCAGTGGAGCC
						Section 16
	(646)	646	660	670		688
BCV N	(625)	TCTAGTGCAAGGATCGCGTAGTAGAGCCAAATCTGGCAACAGAA				
MHV N	(636)	AAATA-----ATCGCG--CTAGAAGCAGTTCCAACAGCGCC				
Avian infectious bronchitis N	(514)	TCATCAGCGGCATCTAG---TAGAGTACCATCCCGTGAGGGTT				
Consensus	(646)	TCAT	GC	G	ATCGCG	TAGAG CA TTCC GC AG G
						Section 17
	(689)	689	700	710	720	731
BCV N	(668)	CCCCTACCTCTGGTGTACAGCTGATATGGCTGATCAAATTGC				
MHV N	(671)	AGCCTGCCCTCTACTGTAAAAGCTGATATGGCCGAAGAAATTGC				
Avian infectious bronchitis N	(554)	CAGCTGGTCTGTAGGAGTGGAGCTGA---AGATGATCTGATTGC				
Consensus	(689)	C	CCTGCCTCTAGTGTA	ACCTGATATGGCTGATCAAATTGC		
						Section 18
	(732)	732	740	750	760	774
BCV N	(711)	TAGTCTTCTTCTGGCAAAACCTGGCAAGGATGGCACTAAGGCA				
MHV N	(714)	TGCTCTTGTTTTGGCTAAGCTCGGTAAAGATGGCGGCCAGGCC				
Avian infectious bronchitis N	(594)	CCGTGCAGCAAAGATTATTCAGGAGCAGCAG---AGGAAGGGT				
Consensus	(732)	T	GTCTTGTT	TGGCTAA	CT	GGCAAGGATGCCAG AAGCC
						Section 19
	(775)	775	780	790	800	817
BCV N	(754)	CAGCAAGTAACCTAAGCAGACTGCCAAAGAAATCAGACA--GAA				
MHV N	(757)	AAGCAAGTAACGAAGCAAGTCCCAAAGAGTCAGGCA--GAA				
Avian infectious bronchitis N	(634)	ACGCGCATTACTAAGCAAAAGGCAGAAAGAGATGGCTCATCGCC				
Consensus	(775)	AAGCAAGTAACCTAAGCAA	TGCCAAAGAAATCAG	CA	GAA	
						Section 20
	(818)	818	830	840	850	860
BCV N	(795)	AATTTTGAATAAGCCCCGCCAGAGAGGAGCCCCAATAAACA				
MHV N	(798)	AATTTTAAACAAGCCTCGGCCAAAGAGGACTCCAACAAGCAG				
Avian infectious bronchitis N	(677)	GATTCGTAAAGCGTAGGGTGCCACCAGGTTATAGAGTAGATCA				
Consensus	(818)	AATTTTGA	AAGCCCCGCCA	AAGAGGA	CC	AATAAACA
						Section 21
	(861)	861	870	880	890	903
BCV N	(838)	TGCACGTGTCAGCAGTGTMTGGGAAGAGAGGCCCCCAATCAGA				
MHV N	(841)	TGCCGAGTGCAGCAGTGTMTGGGAAGAGAGGCCCCCAATCAGA				
Avian infectious bronchitis N	(720)	AGTTTTTGGCCCTCGTACTAAACGTAAAGAGGGT-----A				
Consensus	(861)	TGC	CTGTGCAGCAGTGTMTGGGAAGAGAGGCCCCCAATCAGA			

FIGURE 3A (contd.)

Section 22							
	(904)	904	910	920	930	946	
BCV N	(881)	ATTTTGGTGGTGGAGAAATGTTAAAACTTGGAACTAGTGACCC					
MHV N	(884)	ATTTTGGAGGCTCTGAAATGTTAAAACTTGGAACTAGTGATCC					
Avian infectious bronchitis N	(755)	ATTTTGGTGATGACAAGATGAATGAGGAAGGTATTAAGGATGG					
Consensus	(904)	ATTTTGGTGGTG	GAAATGTTAAAACTTGGAACTAGTGATCC				
Section 23							
	(947)	947	960	970	989		
BCV N	(924)	ACAGTTGCCCATTCCTTGCAGAAC - TCGACCCACAGCTGGTGCC					
MHV N	(927)	ACAGTTCCCATTCCTTGCAGAGT - TGGCTCCAAGAGTTGGTGCC					
Avian infectious bronchitis N	(798)	GC - GTGTTACAGCAATGCTCAAGCTTACACCAAGCCACATGC					
Consensus	(947)	ACAGTTCCCATTCCTTGCAGAAC	T	GCACCAACAGCTGGTGCC			
Section 24							
	(990)	990	1000	1010	1020	1032	
BCV N	(966)	GTCTTCTTTGGATCAAGATTAGAGTTGGCCAAAGTGCAGAAAT					
MHV N	(969)	CTTCTCTTTGGATCTAAATTAGAAATGGTCAAAA - - - AGAAT					
Avian infectious bronchitis N	(840)	TTGTCTTTTGGGAAGTAGAGT - GAC - - - GGCACAG - - - - -					
Consensus	(990)	TTTTTCTTTGGATCTAGATTAGA	TTGGCCAAAG	AGAAT			
Section 25							
	(1033)	1033	1040	1050	1060	1075	
BCV N	(1009)	TTGTCTGGGAATCTTGACGAGCCCCAGGAAGGATGTTTATGAAT					
MHV N	(1009)	T - - - CTGGTGGTGGTGCATCAACCCACCAAGATGTTGATGAGC					
Avian infectious bronchitis N	(871)	- - - - CT - - - TCAACGAGATGGGCTTC - - - ACCTTAGATTTCGAT					
Consensus	(1033)	T	CTGGT	ATCCTGATGAGCCCC	AA	GATGT	TATGAAT
Section 26							
	(1076)	1076	1090	1100	1118		
BCV N	(1052)	TGCGGTATAATCGTGCAATTAGATTGACAGTACACTTTTCAGG					
MHV N	(1049)	TGCAATATTTCAGGTGCAGTTAGATTGATAGTACTCTACCTGG					
Avian infectious bronchitis N	(905)	TT - ACTACTGGGTGGC - - - TAGAGATGACCCGCAGTTTGATAA					
Consensus	(1076)	TGCACTATT	TGGTGCA	TTAGATTGACAGTAC	CTT	CTGG	
Section 27							
	(1119)	1119	1130	1140	1150	1161	
BCV N	(1095)	TTTTGAGACCATATA - - - - ATGAAGGTGTTGAATGAGAAATTTGAA					
MHV N	(1092)	TTTTGAGACTATC - - - - ATGAAAGTGTGGAATGAGAAATTTGAA					
Avian infectious bronchitis N	(945)	TTATGTAAAAATTTGTGATGAGTGTCTTGTGCTGTAG - - GAA					
Consensus	(1119)	TTTTGAGAC	AT	ATGAA	GTCTTGAATGAGAAATTTGAA		
Section 28							
	(1162)	1162	1170	1180	1190	1204	
BCV N	(1134)	TGCATATCAACAACAAGATGGTAT - GATGAATATGA - GTCCAA					
MHV N	(1131)	TGCCTACCAGAAGGATGGTGGTGCAGATGTGG - TGA - GGGCAA					
Avian infectious bronchitis N	(986)	CACGTCCAAAGGAGGAAGTTGTAA - CACCAAGTCCACGGCAA					
Consensus	(1162)	TGC	TACCAA	AACAAGGTGGTA	GATGAA	TGA	GCCCAA

FIGURE 3A (contd.)

						Section 29
	(1205)	1205	1210	1220	1230	1247
BCV N (1175)		AACCACAGCGTCA	---	GCGTGGTCAG	---	AAGAATGGACAAG
MHV N (1172)		AGCCCCAAGAAAAGGGCGTAGACAGGCTCAGGAAAAGA	-	AAG		
Avian infectious bronchitis N (1028)		ATTCAAGAGCTGC	--	TACAAGAACAAG	-	TTCTCCAGCGCCAAG
Consensus (1205)		A CCACAACGT A		GCGTGGACAGG T A	GAA	GACAAG
						Section 30
	(1248)	1248	1260	1270	1280	1290
BCV N (1211)		GAGAAAATCATAATATAAGTGTTCAGCGCGTAAAAGCCGTGT				
MHV N (1214)		ATGAAGTAGATAATGTAAGCSTTGCAAGCCCCAAAAGCTCTGT				
Avian infectious bronchitis N (1068)		ACAACAGCGTCAAAAAGAGGAGAAGAGTCAAAGAAAGCAGGAT				
Consensus (1248)		A GAAA GATAATATAAG GTTGCAA GCC AAAAGC GTGT				
						Section 31
	(1291)	1291	1300	1310	1320	1333
BCV N (1254)		GCAGCAAAATTAAGAGTAGAGAGTTGACTGCAGA	---	GGACATC		
MHV N (1257)		GCAGCGAAATGTAAGTAGAGAATTAAACCCAGA	---	GGATAGA		
Avian infectious bronchitis N (1111)		GATGAAGTAGATAAG	---	GCAATGACCTCAGATGAGGAGAGG		
Consensus (1291)		GCAGCAAAATATAAGTAGAGAATTGACC CAGA		GGA AG		
						Section 32
	(1334)	1334	1340	1350	1360	1376
BCV N (1294)		AGCCTTCT	---	TAAGAAGATGGATGA	-----	GCCCTATA
MHV N (1297)		AGTGTGTGGCTCAGATCCTTGATGATGGCGTAGTGCCAGATG				
Avian infectious bronchitis N (1150)		AACAATGCACAGCTGGAATTTGATGATGAACCCAAGGTGATTA				
Consensus (1334)		AGCCTT T TCAGAA TTGATGATG				GCC ATA
						Section 33
	(1377)	1377	1390	1400		1414
BCV N (1325)		CT	---	GAAGACACCTCAGAAATATAA	-----	
MHV N (1340)		GGTTAGAAGATGACTCTAATGTGTAA	-----			
Avian infectious bronchitis N (1193)		ACTGGGGGGATTTCAGCACTTGGAGAGAATGAGTTGTAA				
Consensus (1377)		T GAAGAT CCTCA ATGTATAA				
BCV N		SEQ ID NO: 9883				
MHV N		SEQ ID NO: 9894				
Avian infectious bronchitis N		SEQ ID NO: 9903				

FIGURE 3B

Section 1						
	(1)	1	10	20	30	41
HOBMPRO	(1)	GATGTGGATGACGTTTAGGTAATCCAAACATTATGAGTAGT				
BCV M	(1)	-----ATGAGTAGT				
MHV M	(1)	-----ATGACTAGT				
Avian infectious brochitis virus M	(1)	-----				
Consensus	(1)	ATGAGTAGT				
Section 2						
	(42)	42	50	60	70	82
HOBMPRO	(42)	AAACTA---CTCCAGGACCAGTTTATCTCTGGACTGCTGA				
BCV M	(10)	GTAAC TA---CACCAGCACCAGTTTACACCTGGACTGCTGA				
MHV M	(10)	ACCACTCAGGCTCCACAGCCTGTTTATCAGTGGACGGCTGA				
Avian infectious brochitis virus M	(1)	--ATGTC---CAACGCGGCAAATTGCAC TCTTGACTG-TGA				
Consensus	(42)	A AACTC CTCCAGCGCCAGTTTATCTCTCTGGACTGCTGA				
Section 3						
	(83)	83	90	100	110	123
HOBMPRO	(80)	TGAAGCTATTAAATTCCCTAAAGGAATGGAATTTTTCTTTGG				
BCV M	(48)	TGAAGCTATTAAATTCCCTAAAGGAATGGAACTTTTCTTTGG				
MHV M	(51)	TGAGGCAATTCGATTCCCTAAGGAATGGAATTTCTCTCFCG				
Avian infectious brochitis virus M	(36)	ACAGTCAGTTGAGCTTTTAAAGAATATAATTTATTATATAA				
Consensus	(83)	TGAGGCTATTAAATTCCTTAAGGAATGGAATTTTTCTTTGG				
Section 4						
	(124)	124	130	140	150	164
HOBMPRO	(121)	GTATTATACTACTTTTTATTACAATCATATTGCAATTTGGA				
BCV M	(89)	GTATTATACTACTTTTTATTACAATCATATTGCAATTTGGA				
MHV M	(92)	GCATTATACTACTTTTTGTTACTATCATACTACAGTTCGGT				
Avian infectious brochitis virus M	(77)	CCGCATTCCCTATTGTTTCTTACTATACTACTTCAGTATGGA				
Consensus	(124)	GTATTATACTACTTTTTATTACTATCATATTGCAGTTTGG				
Section 5						
	(165)	165	170	180	190	205
HOBMPRO	(162)	TATACAAGTCGGAGTATGTTTGTTTATGTTATTAAAGATGAT				
BCV M	(130)	TATACAAGTCGCAGTATGTTTGTTTATGTTATTAAAGATGAT				
MHV M	(133)	TACACGAGCCGTAGCATGTTTGTTTATGTTTGGAATAATGAT				
Avian infectious brochitis virus M	(118)	TATGCCACAAGGAGTCGGTTTAAATTACATAATGAAAATGAT				
Consensus	(165)	TATACAAGTCGCAGTATGTTTGTTTATGTTATTAAAGATGAT				
Section 6						
	(206)	206	220	230		246
HOBMPRO	(203)	TATTTTGTGGCTTATGTGGCCCTTACTATAATCTTAACTA				
BCV M	(171)	CATTTTGTGGCTTATGTGGCCCTTACTATCATCTTAACTA				
MHV M	(174)	ACTTTTGTGGCTTATGTGGCCACTAACTATGTTTGTGTGA				
Avian infectious brochitis virus M	(159)	AGTGTTATGGTGCTTTTGGCCCTTAAACATTGCAGTAGGTG				
Consensus	(206)	AATTTTGTGGCTTATGTGGCCCTTACTATTGTCTTAAGTA				

FIGURE 3B (contd.)

Section 7				
	(247) 247	260	270	287
HOBMPRO (244)	TTTTCAATTGCGTATACGCATTGAATAATGTGTATCTTGGC			
BCV M (212)	TTTTCAATTGCGTGTATGCGTTGAATAATGTGTATCTTGGC			
MHV M (215)	TTTTTAAC TGCGTCTATGCGCTAAATAATGTGTATCTTGGG			
Avian infectious brochitis virus M (200)	TAATTTTCATGTATATATCCACCAAATACAGGAGGTCTTGTG			
Consensus (247)	TTTTTAATTGCGTATATGCGTTGAATAATGTGTATCTTGGC			
Section 8				
	(288) 288	300	310	328
HOBMPRO (285)	CTTCTATAGTTTTTTACCATAGTGGCCATTATTATGTGGAT			
BCV M (253)	TTTCTATAGTTTTCACTATAGTGGCCATTATCATGTGGAT			
MHV M (256)	TTTTCTATAGTGTTTACTATAGTGTCCATTATAATGTGGAT			
Avian infectious brochitis virus M (241)	GCAGCGAAAATACTTACAGTGGTTGCGTGTCTGTCTTTTGA			
Consensus (288)	TTTTCTATAGTTTTTACTATAGTGGCCATTAT ATGTGGAT			
Section 9				
	(329) 329	340	350	369
HOBMPRO (326)	TGTGTATTTTGTGAATAGTATCAGGTTGTTTATTAGAACTG			
BCV M (294)	TGTGTATTTTGTGAATAGTATCAGGTTGTTTATTAGAACTG			
MHV M (297)	TATGTATTTTGTGAATAGCATCAGGTTGTTTATTAGAACTG			
Avian infectious brochitis virus M (282)	AGGATATTGGATTTCAGAGTATCAGACTCTTTAAGCGGGGTG			
Consensus (329)	TGTGTATTTTGTGAATAGTATCAGGTTGTTTATTAGGACTG			
Section 10				
	(370) 370	380	390	400 410
HOBMPRO (367)	GAAGTTTTTGGAGTTTCAACCCAGAAACAAACAACTTGATG			
BCV M (335)	GAAGTTGGTGGAGTTTGAACCCAGAAACAAACAACTTGATG			
MHV M (338)	GCAGCTGGTGGAGCTTCAACCCGAAACAAACAACTTAATG			
Avian infectious brochitis virus M (323)	GGCAATGGTGGGCATTTAACCCTGAGTCTAA - - - - TGCCG			
Consensus (370)	GAAGTTGGTGGAGTTTCAACCCAGAAACAAACAACTTGATG			
Section 11				
	(411) 411	420	430	440 451
HOBMPRO (408)	TGTATAGATATGAAAGGAACAATGTATGTTAGGCCGATAAT			
BCV M (376)	TGTATAGATATGAAGGGAAGGATGTATGTTAGGCCGATAAT			
MHV M (379)	TGTATAGATATGAAAGGTAAGTGTATGTTAGGCCGATAAT			
Avian infectious brochitis virus M (359)	T - - - - AGGT - TCAATACCTCCTATCTA - - - ATGCTCAACAAT			
Consensus (411)	TGTATAGATATGAAAGGTACTATGTATGTTAGGCCGATAAT			
Section 12				
	(452) 452	460	470	480 492
HOBMPRO (449)	TGAGGACTATCATACTCTGACGGTCACAATAATACGCGGCC			
BCV M (417)	TGAGGACTACCATACCTTACGGTCACAATAATACGTTGCTC			
MHV M (420)	AGAGGATTACCATACACTAACAGCCACTATCATTGCTGCTC			
Avian infectious brochitis virus M (392)	GTAATTTTGGTATAGA - - GAGTGTGCCAAT - - - - - GGTG			
Consensus (452)	TGAGGATTACCATACACTGACGGTCACAATAATACGTGGTC			

9/199

FIGURE 3B (contd.)

Section 13					
(493)	493	500	510	520	533
HOBMPRO (490)	ATCTTTACATTCAAGGTATAAACTAGGTACTGGCTATTCT				
BCV M (458)	ATCTTTACATGCAAGGTATAAACTAGGTACTGGCTATTCT				
MHV M (461)	ACCTCTATATGCAAGGTGTTAAGCTAGGCACTGGCTTCTCT				
Avian infectious brochitis virus M (424)	CTTTCT - - - - CCAATTATAAAGAATGGAGTTCTTTATTGT				
Consensus (493)	ATCTTTACATGCAAGGTATAAAGCTAGGTACTGGCTATTCT				
Section 14					
(534)	534	540	550	560	574
HOBMPRO (531)	TGGGCAGATTTCGCCAGCTTATATGAGTGTGCTAAGGTAC				
BCV M (499)	TTCTCAGATTTCGCCAGCTTATGTGACTGTGGCTAAGGTCTC				
MHV M (502)	TTGTCTGATTTCGCTGCTTATGTTACAGTTGCTAAGGTGTC				
Avian infectious brochitis virus M (460)	GAGGGTCAGTGGCTTGC - - - - TAAATGTGAACCAAGACCAAC				
Consensus (534)	TTGTCTGATTTCGCTGCTTATGTGACTGTTGCTAAGGTCTC				
Section 15					
(575)	575	580	590	600	615
HOBMPRO (572)	ACACCTGTGCACATATAAGCGTGGTTTTCTTGACAAGGATAA				
BCV M (540)	ACACCTGTGCACATATAAGCGTGGTTTTCTTGACAAGGATAA				
MHV M (543)	TGACCTTTGGCACTTATAAGCGCGCATTCCTAGACAAGGTAG				
Avian infectious brochitis virus M (496)	TTGCCTAAAGACATATTTG - - - - - TTGCCCCACCAAGATAG				
Consensus (575)	TCACCTGTGCACATATAAGCGTGGTTTTCTTGACAAGATAG				
Section 16					
(616)	616	630	640	656	
HOBMPRO (613)	GCGATACTAGTGGTTTTGCTGTTTATGTTAAGTCCAAAGTC				
BCV M (581)	GCGATACTAGTGGTTTTGCTGTTTATGTTAAGTCCAAAGTC				
MHV M (584)	ACGGTGTAGCGGTTTTGCTGTTTATGTTAAGTCCAAAGTC				
Avian infectious brochitis virus M (531)	ACG-TAATA - - - - - TCTACCGTATG-GTGCAG - - - AAATAC				
Consensus (616)	GCGATACTAGTGGTTTTGCTGTTTATGTTAAGTCCAAAGTC				
Section 17					
(657)	657	670	680	697	
HOBMPRO (654)	GGTAATTACCGACTGCCATCAACCCAAAAGGGTCTGGGCAT				
BCV M (622)	GGTAATTACCGACTGCCATCAACCCAAAAGGGTCTGGGCAT				
MHV M (625)	GGAAATTACCGACTGCCCTCAAATAAACCGAQT - - - GGCA				
Avian infectious brochitis virus M (562)	ACTGGTGACC-AAAGCGGAAATAAGAAAAGGTTTGCTACA-				
Consensus (657)	GGTAATTACCGACTGCCATCAACCCAAAAGGGTCTGGGCAT				
Section 18					
(698)	698	710	720	738	
HOBMPRO (695)	GGACACCGCATTTGTTGAGAAATAATATCTAAATTTTAAGGA				
BCV M (663)	GGACACCGCATTTGTTGAGAAATAATATCTAA - - - - -				
MHV M (663)	GGACACCGCATTTGTTGAG - - - - - ATCTAA - - - - -				
Avian infectious brochitis virus M (601)	- - - - -				
Consensus (698)	GGACACCGCATTTGTTGAGAAATAATATCTAA				
Section 19					
(739)					
HOBMPRO (736) TG	SEQ ID NO: 9912				
BCV M (694) --	SEQ ID NO: 9884				
MHV M (688) --	SEQ ID NO: 9895				
Avian infectious brochitis virus M (601) --	SEQ ID NO: 9904				
Consensus (739)					

10/199

FIGURE 3C

		Section 1					
	(1)	1	10	20	30	40	53
HOBHEGA	(1)	CTAAACTCAGTGAAAATGTTTTTGCTTCCTAGATTTATTCTAGTTAGCTGCAT					
BCV HE	(1)	CTAAACTCAGTGAAAATGTTTTTGCTTCCTAGATTTGTTCTAGTTAGCTGCAT					
MHV HE	(1)	-----					
Consensus	(1)	CTAAACTCAGTGAAAATGTTTTTGCTTC TAGATTT TTCTAGTTAGCTGCAT					
		Section 2					
	(54)	54	60	70	80	90	106
HOBHEGA	(54)	AATTGGTAGCTTAGGTTTTTACAA CCTCCTACCAATGTTGTTTCGGATGTAA					
BCV HE	(54)	AATTGGTAGCCTAGGTTTTGACAATCCTCGTACCAATGTTGTTTCGGATTTAA					
MHV HE	(1)	-----					
Consensus	(54)	AATTGGTAGC TAGGTTTT ACAA CCTCCTACCAATGTTGTTTCGCAT TAA					
		Section 3					
	(107)	107	120	130	140	150	159
HOBHEGA	(107)	ATGGAGATTGGTTTTTATTTGGTGACAGTCGTTTCAGATTGTAATCATATTGTT					
BCV HE	(107)	ATGGAGATTGGTTTTTATTTGGTGACAGTCGTTTCAGATTGTAATCATATTGTT					
MHV HE	(1)	-----					
Consensus	(107)	ATGGAGATTGGTTTTTATTTGGTGACAGTCGTTTCAGATTGTAATCAT TTGTT					
		Section 4					
	(160)	160	170	180	190	200	212
HOBHEGA	(160)	AATATCAACCCGCATAATTAATCTTATATGGAGCTTAATCCTGTTCTGTGTGA					
BCV HE	(160)	ACTACCAACCCGCCTAATTATTCTTATATGGACCTTAATCCTGCCTTGTGTGG					
MHV HE	(1)	-----					
Consensus	(160)	A TA CAACCCCC TAATTATTCTTATATGGACCTTAATCCTG TGTGTG					
		Section 5					
	(213)	213	220	230	240	250	265
HOBHEGA	(213)	TTCTGGTAAAATATCATCTAAAGCTGGCAACTCCATTTT TAGGAGTTTTCAGT					
BCV HE	(213)	TTCTGGTAAAATATCATCTAAAGCTGGCAACTCCATTTT TAGGAGTTTTCAGT					
MHV HE	(1)	-----					
Consensus	(213)	TTCTGGTAAAATATCATCTAAAGCTGGCAACTCCATTTT TAGGAGTTTTCAGT					
		Section 6					
	(266)	266	280	290	300	310	318
HOBHEGA	(266)	TTACCGATTTTTTATAATTACACAGGCGAAGGTCAACAAATTATTTT TATGAG					
BCV HE	(266)	TTACCGATTTTTTATAATTACACAGGCGAAGGTCAACAAATTATTTT TATGAG					
MHV HE	(1)	-----					
Consensus	(266)	TTACCGATTTTTTATAATTACACAGGCGAAGGTCAACAAATTATTT TATGAG					
		Section 7					
	(319)	319	330	340	350	360	371
HOBHEGA	(319)	GGTGTTAATTTTACGCCTTATCATGCCTTTAAATGCAACCGTTCTGGTAGTAA					
BCV HE	(319)	GGTGTTAATTTTACGCCTTATCATGCCTTTAAATGCAACCGTTCTGGTAGTAA					
MHV HE	(1)	-----					
Consensus	(319)	GGTGTTAATTTTACGCCTTATCATGCCTTTAAATGCA C TTCTGGTAGTAA					

FIGURE 3C (contd.)

							Section 8
	(372)	372	380	390	400	410	424
HOBHEGA	(372)	TGATATTTGGATGCAGAAATAAAGGCTTGT	TTTATACTCAGGTTTATAAGAATA				
BCV HE	(372)	TGATATTTGGATGCAGAAATAAAGGCTTGT	TTTACACTCAGGTTTATAAGAATA				
MHV HE	(1)	-----ATGGGCAATAAAGCTCGATTTTAT	GGCCGACTGTATGAGAAGA				
Consensus	(372)	TGATATTTGGATGCAGAAATAAAGGCTTGT	TTTATACTCAGGTTTATAAGAATA				
							Section 9
	(425)	425	430	440	450	460	477
HOBHEGA	(425)	TGGCTGTGTATCGCAGCCTTACTTTTGTTAATGTACCATATGTTTATAATGGC					
BCV HE	(425)	TGGCTGTGTATCGCAGCCTTACTTTTGTTAATGTACCATATGTTTATAATGGC					
MHV HE	(44)	TGGCCCAATATAGGAGCCTATCGTTTGTTAATGTGTCTTATGCCCTATGGAGGT					
Consensus	(425)	TGGCTGTGTATCGCAGCCTTACTTTTGTTAATGTACCATATGTTTATAATGGC					
							Section 10
	(478)	478	490	500	510	520	530
HOBHEGA	(478)	TCTGCACAATCTACAGCCTTTTGTAATCTGGTAGTTTACTCCTTAATAACCC					
BCV HE	(478)	TCTGCACAATCTACAGCCTTTTGTAATCTGGTAGTTTACTCCTTAATAACCC					
MHV HE	(97)	AATGCAAAGCCCGCCTCGATTGCAAAGACAATACTTTAACACTCAATAACCC					
Consensus	(478)	TCTGCACAATCTACAGCCTTTTGTAATCTGGTAGTTTACTCCTTAATAACCC					
							Section 11
	(531)	531	540	550	560	570	583
HOBHEGA	(531)	TGCATATATAGCTCCTCAAGCTAACTCTGGGGATTATTATTATAAGGTTGAAG					
BCV HE	(531)	TGCATATATAGCTCGTGAAGCTAATTTTGGGGATTATTATTATAAGGTTGAAG					
MHV HE	(150)	CACCTTCATATCGAAGGAGTCTAATTATGTTGATTATTACTATGAGAGTGAGG					
Consensus	(531)	TGCATATATAGCTC TGAAGCTAATT TGGGGATTATTATTATAAGGTTGAAG					
							Section 12
	(584)	584	590	600	610	620	636
HOBHEGA	(584)	CTGATTTTATTATTGTCAGGTTGTGACGAGTATATCGTACCACCTTTGTATTTT					
BCV HE	(584)	CTGATTTTATTATTGTCAGGTTGTGACGAGTATATCGTACCACCTTTGTATTTT					
MHV HE	(203)	CTAATTTTACACTAGAAAGGTTGTGATGAATTTATAGTACCGCTCTGTGGTTTT					
Consensus	(584)	CTGATTTTATTATTGTCAGGTTGTGACGAGTATATCGTACCACCTTTGTATTTT					
							Section 13
	(637)	637	650	660	670		689
HOBHEGA	(637)	AACGGCAAGTTTTTG-----TCCAATACA-----AAGTATTATGATGA					
BCV HE	(637)	AACGGCAAGTTTTTG-----TCCAATACA-----AAGTATTATGATGA					
MHV HE	(256)	AATGGCCATCCCAAGGGCAGCTCTTCGGATGCTGCCAATAAATACTACTCA					
Consensus	(637)	AACGGCAAGTTTTTG TCCAATACA AAGTATTATGATGA					
							Section 14
	(690)	690	700	710	720	730	742
HOBHEGA	(675)	TAGTCAATATTATTTTAATAAAGACACTGGTGTTATTTATGGTCTCAATTCTA					
BCV HE	(675)	TAGTCAATATTATTTTAATAAAGACACTGGTGTTATTTATGGTCTCAATTCTA					
MHV HE	(309)	CTCTCAGAGTTACTATAATATGGATATTGGTGTCTTATATGGGTTCAATTCTA					
Consensus	(690)	TAGTCAATATTATTTTAATAAAGACACTGGTGTTATTTATGGTCTCAATTCTA					

12/199

FIGURE 3C (contd.)

Section 15									
	(743)	743	750	760	770	780	795		
HOBHEGA	(728)	C	-----	AGAAACCATTA	CCA-----	CTGGTTTTGATCTT	AAATTGTTAT		
BCV HE	(728)	C	-----	TGAAACCATTA	CCA-----	CTGGTTTTGACTTT	AAATTGTCAI		
MHV HE	(362)	C	CTTG	GATGTTGGCAACACTG	CTAAGGATC	CGGGTCTTGATCT	CACCTGCAGG		
Consensus	(743)	C		TGAAACCATTA	CCA	CTGGTTTTGATCTT	AAATTGT	AT	
Section 16									
	(796)	796	810	820	830	848			
HOBHEGA	(766)	TATTTAGTTTTAC	CCTCTGGTAATTATTTAGCCATTTCAA	ATGAGCTATTGTT					
BCV HE	(766)	TATTTAGTTTCTA	CCTCTGGTAATTATTTAGCCATTTCAA	ATGAGCTATTGTT					
MHV HE	(415)	TATCTTGCA	TGACTCCTGGTAATTATAAGGCTGTGT	CCTTAGAATATTGTT					
Consensus	(796)	TATTTAGTTTTAC	CCTCTGGTAATTATTTAGCCATTTCAA	ATGAGCTATTGTT					
Section 17									
	(849)	849	860	870	880	890	901		
HOBHEGA	(819)	AACTGTTCC	TACGAAAGCAATCTGTCTTAATAAGCGTAAGGATTTTACGCCTG						
BCV HE	(819)	AACTGTTCC	TACTAAAGCAATCTGTCTTAATAAGCGTAAGGATTTTACGCCTG						
MHV HE	(468)	AAGCTTACCCT	CAAAGGCTATTTGCCATCCATAAGACAAAGCGCTTTATGCCG						
Consensus	(849)	AACTGTTCC	TAC	AAAGCAATCTGTCTTAATAAGCGTAAGGATTTTACGCCTG					
Section 18									
	(902)	902	910	920	930	940	954		
HOBHEGA	(872)	TACAGGTTGTTG	ATTTCGCGGTGGAACAATGCCAGGCAGTCTGATAACATGACG						
BCV HE	(872)	TACAGGTTGTTG	ATTTCGCGGTGGAACAATGCCAGGCAGTCTGATAACATGACG						
MHV HE	(521)	TGCAGGTAGTTG	ACTCAAGGTGGAGTAGCATGCCGAGTCAGACAATATGACC						
Consensus	(902)	TACAGGTTGTTG	ATTTCGCGGTGGAACAATGCCAGGCAGTCTGATAACATGACG						
Section 19									
	(955)	955	960	970	980	990	1007		
HOBHEGA	(925)	GCGGTTGCTTG	TCAACCTCCGTACTGTTATTTTCGTAATCTACTACCACTA						
BCV HE	(925)	GCAGTTGCTTG	TCAACCCCCGTACTGTTATTTTCGTAATCTACTACCACTA						
MHV HE	(574)	GCTGCAGCC	CGTCAGCTGCCATATTGTTTCTTTCCGCAACACATCTGCGAATTA						
Consensus	(955)	GC	GTTGCTTGTC	AACC	CGTACTGTTATTTTCGTAATCTACTACCACTA				
Section 20									
	(1008)	1008	1020	1030	1040	1050	1060		
HOBHEGA	(978)	TGTTGGTGTTT	---ATGATATTAATCATGGAGATGCTGGTTTTACTAGCATAC						
BCV HE	(978)	TGTTGGTGTTT	---ATGATATTAATCATGGGATGCTGGTTTTACTAGCATAC						
MHV HE	(627)	TAGTGGTGG	CACACATGATGCGCACCATGGTGATTTTCATTTCAAGGCAGTTAT						
Consensus	(1008)	TGTTGGTGTTT	ATGATAT	AATCATGG	GATGCTGGTTTTACTAGCATAC				
Section 21									
	(1061)	1061	1070	1080	1090	1100	1113		
HOBHEGA	(1028)	TTAGTGGTTTG	TTATATAATTCACCTTGTTTTTTCGCAGCAAGGCGTTTTTAGG						
BCV HE	(1028)	TCAGTGGTTTG	TTATATGACCTCACCTTGTTTTTTCGCAGCAAGGCGTTTTTAGG						
MHV HE	(680)	TGTCTGGTTTG	TTATATAAATGTTTCTGTATTGCCAGCAGGGTGCATTTCTT						
Consensus	(1061)	T	AGTGGTTTG	TTATATAATTCACCTTGTTTTTTCGCAGCAAGGCGTTTTTAGG					

13/199

FIGURE 3C (contd.)

							Section 22
(1114)	1114	1120	1130	1140	1150	1166	
HOBHEGA (1081)	TATGATAAATGTTAGCAGTGTCTGGCCTCTCTACCCCTATGGCAGATGTCCCAG						
BCV HE (1081)	TATGATAAATGTTAGCAGTGTCTGGCCTCTCTACCCCTATGGCAGATGTCCCCTAC						
MHV HE (733)	TATAATAATGTTAGTTCCTCTTGGCCAGCCTATGGGTACGGTCATTGTCCAAC						
Consensus (1114)	TATGATAAATGTTAGCAGTGTCTGGCCTCTCTACCC	TATGGCAGATGTCC	AC				
							Section 23
(1167)	1167	1180	1190	1200		1219	
HOBHEGA (1134)	TGCTGCTGATATTAATAACCCGTGATTACCCATTGTGTGTATGATCCGCTAC						
BCV HE (1134)	TGCTGCTGATATTAATAACCCGTGATTACCCATTGTGTGTATGATCCGCTAC						
MHV HE (786)	GGCAGCTAACATTGGTTA - - - TATGGCACCCTGTTTGTATCTATGACCCCTCTCC						
Consensus (1167)	TGCTGCTGATATTAATAACCCGTGATGTACCTATTTGTGTGTATGATCCGCTAC						
							Section 24
(1220)	1220	1230	1240	1250	1260	1272	
HOBHEGA (1187)	CAGTTATTTTGCTTGGCATTCTTTTGGGCGTTGCGGTCATAATTATTGTAGTT						
BCV HE (1187)	CAATTATTTTGCTTGGCATTCTTTTGGGCGTTGCGGTCATAATTATTGTAGTT						
MHV HE (836)	CGGTCATACTGCTAGGTGTGTTATTGGGTATAGCTGTGTTGATTATTGTGTTT						
Consensus (1220)	CAGTTATTTTGCTTGGCATTCTTTTGGGTGTTGCGGTCATAATTATTGTAGTT						
							Section 25
(1273)	1273	1280	1290	1300	1310	1325	
HOBHEGA (1240)	TTGTTGTTATATTTTATGGTGGATAAATGGTACTAGGCTGCATGATGCTTAGAC						
BCV HE (1240)	TTGTTGTTATATTTTATGGTGGATAAATGGTACTAGGCTGCATGATGCTTAGAC						
MHV HE (889)	TTGATGTTTATTTTATGACGGATAGCGGTGTTAGATTGCATGAGGCATAA - -						
Consensus (1273)	TTGTTGTTATATTTTATGGTGGATAAATGGTACTAGGCTGCATGATGCTTAGAC						
							Section 26
(1326)	1326	1337					
HOBHEGA (1293)	CATAATCTAAAC		SEQ ID NO: 9913				
BCV HE (1293)	CATAATCTAAAC		SEQ ID NO: 9885				
MHV HE (940)	-----		SEQ ID NO: 9896				
Consensus (1326)	CATAATCTAAAC						

14/199

FIGURE 4**FIGURE 4A**

					Section 1
	(1)	1	10	20	39
avian infectious bronchitis pol 1ab	(1)	-----	-----	-----	-----
bovine coronavirus pol 1ab	(1)	MSKLNKYGLELHWAFEPWMEFEDAEKIDNRSSSEVDIV			
Human corona 229E pol 1ab	(1)	-----	-----	MACNRVTLAVASDSEISANG	
Murine hepatitis pol 1ab	(1)	MAKMGKYGGLGFKWAFEPFWMPLNASEKIDGNPERSEEDGF			
Consensus	(1)	MAKI KYGL	WAFEPW	NA EKL NPDSE D	
					Section 2
	(40)	40	50	60	78
avian infectious bronchitis pol 1ab	(1)	-----	-----	-----	-----
bovine coronavirus pol 1ab	(40)	CSTTAOKTETGGICPENHYMDCRRLDKQEGCVQSSTLR			
Human corona 229E pol 1ab	(21)	CSTIAQAARRYSEAAASNGFACRFVSLDQDCIVGIADD			
Murine hepatitis pol 1ab	(40)	CPSAAQEPKVKCKTLVNHVRVNGSRIPALECCVQSATIR			
Consensus	(40)	CST AQ LK G	NHVRV C RLL	LECCVQSATIR	
					Section 3
	(79)	79	90	100	117
avian infectious bronchitis pol 1ab	(1)	-----	-----	-----	-----
bovine coronavirus pol 1ab	(79)	ELVMNTRPYDLEVLLODALOSREAVLVTEPLGMSLEACY			
Human corona 229E pol 1ab	(60)	TYVMGLHGNOTLFCNIMKFSDEPFMIHG-----WLVEFS			
Murine hepatitis pol 1ab	(79)	DEFDDEDPKVEASTMMALQFGSAVLVKRSKRISLOANT			
Consensus	(79)	DIVM FN LE	IMALQ R AVL V P	LSI AFS	
					Section 4
	(118)	118	130	140	156
avian infectious bronchitis pol 1ab	(1)	-----	-----	-----	-----
bovine coronavirus pol 1ab	(118)	VRGCNPNMTMGLERRRSVNTGRCAYNKHVAYOQYMID			
Human corona 229E pol 1ab	(93)	NSNYLLEEDVVFGR-----GGNVITYTDQYLCGADG			
Murine hepatitis pol 1ab	(118)	NLCVLPKTAAMGLKRVCLCNTRECSCDANVAEHLTVQ			
Consensus	(118)	N G LP SF MGLFRR	LCNTG CAV	HVAYLLF D	
					Section 5
	(157)	157	170	180	195
avian infectious bronchitis pol 1ab	(24)	PEOLCDALFFETSHNPKDYADAFVROKEDRSLOTGKQF			
bovine coronavirus pol 1ab	(157)	PAGVCFGAGQEVGVLPDAFMPVQSRKPTVEWVMYLRKC			
Human corona 229E pol 1ab	(126)	KPVMSEDLWQEVVHEGENEELITNGHTYVCAMITKRKPL			
Murine hepatitis pol 1ab	(157)	PDGVCLNGRPLICNEVPVTAPEYAKOWLOPMSTLLRKG			
Consensus	(157)	PDGVCDGLGQFVGWFIPL	AIPINARQFI	PWLI LKK	
					Section 6
	(196)	196	210	220	234
avian infectious bronchitis pol 1ab	(63)	KEET-----VC--GLFLLKGVDKITPGVPARV			
bovine coronavirus pol 1ab	(196)	GENG-AYNKDHKRGGEFHVYNFKVFDAYDLVHDEPKGKE			
Human corona 229E pol 1ab	(165)	DKKR-----Q--NNLALFEEI EYMHGDALHTLR			
Murine hepatitis pol 1ab	(196)	GNKGSVTSGHFRRAVTMPVYDFNVEQACEEVHLNPKGKY			
Consensus	(196)	GFKG	KRA M VYNL	VEDA DLVHDAPKKGKE	

15/199

FIGURE 4A (contd.)

						Section 7
	(235)	235	240	250	260	273
avian infectious bronchitis pol 1ab	(88)	LKATSKLADLEDIFGVSPHARNYRELLKTACQWSLTVEA				
bovine coronavirus pol 1ab	(234)	SKKAYALIRGYRGVKPLLYVDOYGCDYTGGLADGLEA YA				
Human corona 229E pol 1ab	(190)	NGSVLEMAKEVKTS SKVVLSDALDKLYKVFGSPVMTNGS				
Murine hepatitis pol 1ab	(235)	SKKAYALLKGYRGVKRIEFVDOYGCDYTGCLAKGLEDYG				
Consensus	(235)	SKKAYALAKGYRGVKPILLVDQYGCLYTGA LA GLT YA				
						Section 8
	(274)	274	280	290	300	312
avian infectious bronchitis pol 1ab	(127)	LDVRAQTLDDEIFDPTETLWLQVAAKIEVSSMAMRRIVGE				
bovine coronavirus pol 1ab	(273)	DKTLEQMKALEPTINSCELPFDVTVAWHVVRDPRYVMRLQ				
Human corona 229E pol 1ab	(229)	NILEAFTKPVFISALVQCTCCTKSWSVGDWTGFKSSCCN				
Murine hepatitis pol 1ab	(274)	DITLSEMKELEPVRDRSDSEVLVAWHVDRDPRRAAMRLQ				
Consensus	(274)	DITLAETKDLFPINSD L DV VAWHVDRDPRKAMRLQ				
						Section 9
	(313)	313	320	330	340	351
avian infectious bronchitis pol 1ab	(166)	VTAKVMDAIGSNLSALFQIVKQQTARIFOKATAIFENVN				
bovine coronavirus pol 1ab	(312)	SASTIRSMAYVANPETEDDCDGSVVIKEEVHMYADDSITL				
Human corona 229E pol 1ab	(268)	VTSNKLGMVPGNVKFGDAMITIQQAGAGIKYFCGMILKF				
Murine hepatitis pol 1ab	(313)	TIATVRCEDYVGOPTEDVVDGDIVVREPAHLLAANAIVK				
Consensus	(313)	VIATVRCVLYVNQPTEDLVDGSSVAREPIKLLAA SIV				
						Section 10
	(352)	352	360	370	380	390
avian infectious bronchitis pol 1ab	(205)	ELPQRTAAIKMAFAKARSTTVVVVERTLVVKEFAGTCL				
bovine coronavirus pol 1ab	(351)	RQHNLVDIMSCFYMEADAVVNATYGVDLKDCGEVMOEGY				
Human corona 229E pol 1ab	(307)	VAN-----LEGVSVWRVTALQSVDCFVASSTEVE				
Murine hepatitis pol 1ab	(352)	RLP---RLVETMLYTDSSVTEFCYKTKICEGGEITQFGY				
Consensus	(352)	RLPN I IL FIEAASVI VIYL KL DCGFISQFGY				
						Section 11
	(391)	391	400	410		429
avian infectious bronchitis pol 1ab	(244)	ASINGAVAKTFFELPNEGFMGSKIETTLAFFKEAAVRYVE				
bovine coronavirus pol 1ab	(390)	IDCEQDIDCDPKGWVPGNMIDGFACTTCGHVYETGDLIAQ				
Human corona 229E pol 1ab	(336)	EEHVNRMDTFCFNVRNMTDECRLAMTGAEMTSNVRQV				
Murine hepatitis pol 1ab	(388)	VDCCGDTCDERGVVAGNMMDGEPGPGCTKNYMPWELEAQ				
Consensus	(391)	IDC GDLCDKFGWVFNMMMDGE CTTLG YESAVRLAQ				
						Section 12
	(430)	430	440	450		468
avian infectious bronchitis pol 1ab	(283)	NIPNAPRGTKGFEVVGNAKGTQVVVRGMNDLTLLDOKA				
bovine coronavirus pol 1ab	(429)	SSGVLPVNPMLHTKSAAGYGGFGCKDSFTLYGQTVVYFG				
Human corona 229E pol 1ab	(375)	ASGVLDISTGWFDVYDDIFAE-----SK-PWEVRKA				
Murine hepatitis pol 1ab	(427)	SSGVLPREGGVLEFQSTDTVN----RESERLYGHAVVPG				
Consensus	(430)	SSGVIPIGTVLFTVSADAFG KDSEFKLYG VV KA				

16/199

FIGURE 4A (contd.)

Section 13						
	(469)	469	480	490	507	
avian infectious bronchitis pol 1ab	(322)	DIPVEFEGWSA	ILDGHL	CYVFRSGDRFYAAP	LSGNFALS	
bovine coronavirus pol 1ab	(468)	GCVYWS-	PARNIWIPI	LKSSVKRSYDGLV	ITGVVGCKAIV	
Human corona 229E pol 1ab	(405)	EDIEGP-	CWSATASAL	KQLKVTIGEL	IREVKSECN	
Murine hepatitis pol 1ab	(462)	SAVYWS-	PCPGMWLE	VHWSSVKSM	GLTYTGVVGCKAIV	
Consensus	(469)	D VYWS	PWSATWIPIL	SSVKSYDGL	YTGVDVGNKAIV	
Section 14						
	(508)	508	520	530	546	
avian infectious bronchitis pol 1ab	(361)	DVHCCERV	VCLSDGVT	PEINDGLILA	ATYSSFSVSELVA	
bovine coronavirus pol 1ab	(506)	KETNLICKA	LYLDYVOHK	CGNIHQRE	DLGVSDVWVHKOLL	
Human corona 229E pol 1ab	(443)	VVGGTLOILAS	MPEKFLNA	FDMFVTA	IQTFVDFCAVETCT	
Murine hepatitis pol 1ab	(500)	QETDAICRSL	YMDYVOHK	CGNLEORATL	GLGDDVMHFOIL	
Consensus	(508)	VT	ICRSLYLDYVQHKCGNL	QRAILGVSDVWHEQLT		
Section 15						
	(547)	547	560	570	585	
avian infectious bronchitis pol 1ab	(400)	ALRKGEPF	KELGHKFVYAKDAAMS	FTEAKAAT	IAADVLR	
bovine coronavirus pol 1ab	(545)	ENRGVYKPL	LENIDYENMRRAKFS	LETEITV	CADGFMPL	
Human corona 229E pol 1ab	(482)	TAGKAFDK	MDYVLLDNALVK	LMTRIKGV	RERGINVK	
Murine hepatitis pol 1ab	(539)	VNRGDYSL	LENDYVVKRR	AEFACK-	EATGGDGMPL	
Consensus	(547)	INRKAY	LENVDLFNARRA	VS KLF	AVCADGLVPLL	
Section 16						
	(586)	586	600	610	624	
avian infectious bronchitis pol 1ab	(439)	EOSARVIA	EDVWSSFTEKS	FEPWKLAYGK	VNRLEEFVKT	
bovine coronavirus pol 1ab	(584)	LDDLVP	RAYGLAVSGQAF	CDYADKTC	HAVVSKSKELLDM	
Human corona 229E pol 1ab	(521)	YATVVG	STEEMKSS-	-----R	VERSTAVLPIANNYSKL	
Murine hepatitis pol 1ab	(577)	LDCLVPR	SYLLKSGQAF	TSMMVN	SHEVTUMCMQALL	
Consensus	(586)	LDSL	VVRAYYLIKSGQAFS	VKISHAVVSIA	EMSKL	
Section 17						
	(625)	625	630	640	650	663
avian infectious bronchitis pol 1ab	(478)	YVCKAQM	STVILAAMV	LGEDIWHLVS-	---QV	IYKLGVL
bovine coronavirus pol 1ab	(623)	SLDSL	SAATHYLN	SKIVDLAQHF	SDFGTS	SPVSKIVHEEK
Human corona 229E pol 1ab	(554)	EDGYT	VMVIGDMAYF	MSDGYER	ELMASPNS	VLLTAMVKPL
Murine hepatitis pol 1ab	(616)	FMHDM	VMATKYVK	KVTGKLAVR	KALGVAVVR	KTEWED
Consensus	(625)	FLD	LSVAI YLAAVIGDLAFLMA	G SVVSKIVHFF		
Section 18						
	(664)	664	670	680	690	702
avian infectious bronchitis pol 1ab	(514)	KVVDF	CDKHMKGF	GVOLKRAKL	IVTETFCV	LKGVAQHCF
bovine coronavirus pol 1ab	(662)	TFTT	STALAFAMV	LEHVHQA	IVVESD	YFVKNLPRYA
Human corona 229E pol 1ab	(593)	FAFN	VNVMGTR	PEKEPTT	VTCE	NLES
Murine hepatitis pol 1ab	(655)	LAVD	IAASAAG	MDCYOLV	NGL	EA
Consensus	(664)	AVDI	ALAFKWL	CFQLL	G FIV	EAVIFFV IPEF

17/199

FIGURE 4A (contd.)

Section 19						
	(703)	703	710	720	730	741
avian infectious bronchitis pol 1ab	(553)	QLLLDAIHSLYKSFKKCALGRTHGDLLEFWKGGVHKIVQD				
bovine coronavirus pol 1ab	(701)	SAMAAQAFERSVAKVLDSTRVTTFIDGLSCPKIGRRRTCLSL				
Human corona 229E pol 1ab	(632)	LDYSIDVIDNEIIVKPNISLCVPLYVRDYVDKWDDEFGRG				
Murine hepatitis pol 1ab	(694)	KNEVDKEKAFERKVLIDSMVSVILSGLTVVKTAASNRVCLA				
Consensus	(703)	VSDAFKSLFKVVKDSISVSII	GLS	FK	G	RICLA
Section 20						
	(742)	742	750	760	770	780
avian infectious bronchitis pol 1ab	(592)	GD-----				
bovine coronavirus pol 1ab	(740)	GSKIYEVEERGLLHSSQLPLDVYDLTMP	SQVQKAKQKPIY			
Human corona 229E pol 1ab	(671)	YS-----				
Murine hepatitis pol 1ab	(733)	GSKVYEVVQKSLSSAYVMPVGCSEATCLVGEIEP-----				
Consensus	(742)	GSKIYEV	L A	LPL	D T	
Section 21						
	(781)	781	790	800	819	
avian infectious bronchitis pol 1ab	(594)	-----EIMFDAHDSVDMEDEGMVQEKSLDFEVED				
bovine coronavirus pol 1ab	(779)	LKSGSGDSESLADSVVEVTTSTMPCCGYSEEPKMAADKICI				
Human corona 229E pol 1ab	(673)	-----NESWFEDDYRAFTSVLEDTDAAVKAAESKA				
Murine hepatitis pol 1ab	(766)	-----AVFEDDVVDVVKAPLTYQGCKEPEESFEKICET				
Consensus	(781)	EDWVVDVVS	A	LT	LGISDPPSIADKICI	
Section 22						
	(820)	820	830	840	858	
avian infectious bronchitis pol 1ab	(623)	DMTEPENQPGHMMVQIEDDGKNYMFFRFKKDENIYYTPMS				
bovine coronavirus pol 1ab	(818)	VDNVYMAKAGDKYYPVVVDG-HVGLLDQAWRVPCAGRRV				
Human corona 229E pol 1ab	(703)	FVDTIMPPCPSELKVLDDGGKIWNGVTKNVNSMRDWLKS				
Murine hepatitis pol 1ab	(798)	VDKLYMAKCGDQFPLVVDNDTGVLDQCWRFFPCAGKKV				
Consensus	(820)	VV	LYMAKCGDIVYPVVVGK	WVGVL	DQ WRVPCAGKKV	
Section 23						
	(859)	859	870	880	897	
avian infectious bronchitis pol 1ab	(662)	QIIGAINVCKAGGKTVTFGETTVQEIIPPPDVVPIKVSIE				
bovine coronavirus pol 1ab	(856)	TEHEQPTVNEEASTPKTKVFMELDKDENTIENTACME				
Human corona 229E pol 1ab	(742)	KENLTQQGLLGTCARFRKRWLGTFLEAYNAFLDTVVSTV				
Murine hepatitis pol 1ab	(837)	EENDKPKVRKTFST-RKIKLTFALDATEDSVLSKACSEF				
Consensus	(859)	LND	P V	KIAST RTIKITFILD	FNSVL	TAVSIF
Section 24						
	(898)	898	910	920	936	
avian infectious bronchitis pol 1ab	(701)	CCGEPWN-----TFKKAYKEPIEVDTDTEVEQLLSV				
bovine coronavirus pol 1ab	(895)	EVDDTVDMEEFYAVVIDAIEPKLSPCKELEGVGAKVSAT				
Human corona 229E pol 1ab	(781)	RTGG-----LTFKLYAFDKPIVIRDIVCKV				
Murine hepatitis pol 1ab	(875)	EVDKDYTLDELLDVLDVAVESTESPECKEHDVIGTKVCAL				
Consensus	(898)	EVGD	V LDE	VVIDAIE	TLSPCKEHDVIGDKVCAV	

18/199

FIGURE 4A (contd.)

						Section 25
	(937)	937	950	960	975	
avian infectious bronchitis pol 1ab	(733)	LYEKMCDLIK	REAPPPPP	ENVALVDKNG	ILDCIKS	
bovine coronavirus pol 1ab	(934)	LQKLEUNSL	LEDEAGFEVL	ASKLYCAFTAP	EDDDFLFE	
Human corona 229E pol 1ab	(807)	ENKTEAEWTE	LFRRNDRIKSE	STTESAYMPIA	BPTHEDI	
Murine hepatitis pol 1ab	(914)	LDRFAGDYVY	FDEGGDEVIA	PRMYCSFSA	PDDEDCMAA	
Consensus	(937)	LNKLEADWLF	LFPEAGEEVI	FSKLYCAFS	APDDDDCIDA	
						Section 26
	(976)	976	990	1000	1014	
avian infectious bronchitis pol 1ab	(772)	CHLIYRDYFS	DDDIFFEDAE	ECDTDSGEAL	ECDTN----	
bovine coronavirus pol 1ab	(973)	SGVEEDDVGE	ETDLIVTSAGE	PCVASEQEE	-----	
Human corona 229E pol 1ab	(846)	EEVELLDAAE	FVEPGCGGLA	VIDEHVFYKA	DGVYYP---	
Murine hepatitis pol 1ab	(953)	DVVDADEIN	QDDDAEDSAV	IVADTQEE	DGVAKGQVEADSE	
Consensus	(976)	DVEDD	EDD	DDSAILAADD	DAEEEG	
						Section 27
	(1015)	1015	1020	1030	1040	1053
avian infectious bronchitis pol 1ab	(807)	-----	SECEEEDE	DTKVLALL	ODPASIKYPL	PLDEE
bovine coronavirus pol 1ab	(1004)	-----	SSEILEDTL	DDGPCVETS	SDSQVEED	VEMSDFADEE
Human corona 229E pol 1ab	(882)	-----	SNGNILPVA	FTKAAAGKVS	FSDDVVKD	IEPMY
Murine hepatitis pol 1ab	(992)	ICVAHTGS	SELAEPDAV	GSOTPTASAE	TEVGEAS	DRE
Consensus	(1015)	S	SEDL	EDD	AAAIQ	AEDVEVDADLE
						Section 28
	(1054)	1054	1060	1070	1080	1092
avian infectious bronchitis pol 1ab	(838)	YSVYNGCIV	HKDAEDV	VNLPSG	-----	-----
bovine coronavirus pol 1ab	(1039)	SVIQDYEN	ACFEFYTTEP	-----	-----	-----
Human corona 229E pol 1ab	(916)	RYKLCEFE	DEKLYDVCEKA	IG	-----	-----
Murine hepatitis pol 1ab	(1031)	GTAEAKAT	VGADAVD	ACPDQVEA	FEIEKVEDS	SILDELQT
Consensus	(1054)	VI	FEVC	DAVDVCP	IG	
						Section 29
	(1093)	1093	1100	1110	1120	1131
avian infectious bronchitis pol 1ab	(860)	-----	-----	-----	-----	EE
bovine coronavirus pol 1ab	(1057)	-----	-----	-----	-----	EFVKV
Human corona 229E pol 1ab	(938)	-----	-----	-----	-----	KKIK
Murine hepatitis pol 1ab	(1070)	ELNAPADK	TYEDVLAF	DAVCSEALS	AFYAVPSDE	THFKV
Consensus	(1093)					KV
						Section 30
	(1132)	1132	1140	1150	1160	1170
avian infectious bronchitis pol 1ab	(862)	TFMVN	-----	-----	NCFEGAVK	PQPQVMDV
bovine coronavirus pol 1ab	(1062)	LDLYVRKAT	RNCWLRSV	LAVMOKL	PCQFKDKN	LQDLWV
Human corona 229E pol 1ab	(942)	HEG	-----	DWDSFCKT	QSALSVVSC	YVNLPTYXI
Murine hepatitis pol 1ab	(1109)	CGFYS	PAIERTN	CWLRSTLI	VMOSTPLE	FRDLQMOKLWL
Consensus	(1132)	DLYP	RNCWLRS	LVMQALPL	FKDLNLQ	LWV

19/199

FIGURE 4A (contd.)

Section 31					
	(1171)	1171	1180	1190	1209
avian infectious bronchitis pol 1ab (884)		LGDWGEAVDAQEQLCQOE	FLQHTFEEPVEN	STGSSKTM	T
bovine coronavirus pol 1ab (1101)		LYKQOYSOLFVDTLVNKT	FLANIVVPQGGYVAD	FAYWELT	
Human corona 229E pol 1ab (972)		YDEEGGNOLSLPVMISEW	LSVQQAQOEATLPDIA	EDMV	
Murine hepatitis pol 1ab (1148)		SYKAGYDQCFVDKLVKS	SVFKSITLPPQGGYVAD	FAYEPE	S
Consensus (1171)		LYK GYAQLFVD LVN	IPLSIILPQGGYVAD	FAYFFLT	
Section 32					
	(1210)	1210	1220	1230	1248
avian infectious bronchitis pol 1ab (923)		EOVVVEDQELPVVEQ	QDVVMYTPTDLEVAKETAE	EMDE	
bovine coronavirus pol 1ab (1140)		LCDWQCVAYNKCINQ	DALKTKGLDAMFFYGDV	VSHVCK	
Human corona 229E pol 1ab (1011)		DOVEEVNSLEDIETV	VKHDVSPFEMPFEELNGL	KIKQ	
Murine hepatitis pol 1ab (1187)		QCSEKAYANWRQLECDME	EKKLOGLDAMFFYGDV	VSHMCK	
Consensus (1210)		DQVF A WKCIECDL	DLKL GLDAMFFYGDV	VSHVCK	
Section 33					
	(1249)	1249	1260	1270	1287
avian infectious bronchitis pol 1ab (962)		FILIFAMPKEEVVSQKDG	AOIKQEPQVVKP	ORE-KK--	
bovine coronavirus pol 1ab (1179)		CGESMVLTDMDVPFETA	HFALKKLECAFI	TKRSVYKAAC	
Human corona 229E pol 1ab (1050)		LDNNCWVNSVMLOIQIT	GILGGDYAMQEF	KMG-----	
Murine hepatitis pol 1ab (1226)		CGNSMTLLS	DIPTLHFGVRDDK	ECAPYTPRKVERAAC	
Consensus (1249)		CGNSM LISVDVPFTL	HGALKDD	FCQFVTPRKVFKAAC	
Section 34					
	(1288)	1288	1300	1310	1326
avian infectious bronchitis pol 1ab (998)		-----	-----	-----	AK
bovine coronavirus pol 1ab (1218)		VVDVNDSHSMAVVDGK	QIDDHRTSITSDK	FDFTIGHGM	
Human corona 229E pol 1ab (1082)		-----	-----	-----	-----
Murine hepatitis pol 1ab (1265)		AVDVNDCHSMAVVEGK	QIDGKVVT	KFIGDKEDFMVGYGM	
Consensus (1288)		VDVND HSMVVDGKQID	VT	DKFDFIIGHGM	
Section 35					
	(1327)	1327	1340	1350	1365
avian infectious bronchitis pol 1ab (1000)		REKVKBATCERPKFLEM	KTCVGDLT	VVIAKALDEFKEFC	
bovine coronavirus pol 1ab (1257)		SFSMTTEETAQLYGSC	ITPNVCFVKGDI	IKVSKRVKAEV	
Human corona 229E pol 1ab (1082)		-----	RVAKMIERCYTALQ	CIRGAMGDVGLCMYRLK	
Murine hepatitis pol 1ab (1304)		TFMSSPFEELAQLYGSC	ITPNVCFVKGDI	IKVRLVNAEV	
Consensus (1327)		SFSMSPFETIAQLYGSC	YTPNVCFVKGDI	IKVLKLVKAEV	
Section 36					
	(1366)	1366	1380	1390	1404
avian infectious bronchitis pol 1ab (1039)		IVNAANEHMTGSGVAKA	IADFCCLD	MEYCEDYVKKHG	
bovine coronavirus pol 1ab (1296)		VVNPNANGHMAHGCGV	AKATAVAAGQO	EVKETTTDMVKS	
Human corona 229E pol 1ab (1114)		DLHTGFMVMDYKCSCT	SGRLLES	AVLFCFTPTTKAFPY	
Murine hepatitis pol 1ab (1343)		IVNPNANGHMAHGAGV	AKAIAE	SALTKETSDMVKAQ	
Consensus (1366)		IVNPNANGHMAHGAGV	AKAIAE	AGA FVKETTTDMVKAH	

FIGURE 4A (contd.)

Section 37					
	(1405)	1405	1410	1420	1430 1443
avian infectious bronchitis pol 1ab (1078)	PQQR	-----	-----	-----	-----
bovine coronavirus pol 1ab (1335)	VGATGDCYVSTGGKLCRTVENVVGP	DARTQCKOSYALLE			
Human corona 229E pol 1ab (1153)	TGLNCNAPRMCTIFRQLGTHIFVQQR	PEP-----VNP			
Murine hepatitis pol 1ab (1382)	VCQVGEQYESAGCKLCKKVLNIVGP	DARGHGKQCYSLTE			
Consensus (1405)	VCQ GDCY S GKKLCK VLNIVGP	DAR GKQ YALLE			
Section 38					
	(1444)	1444	1450	1460	1470 1482
avian infectious bronchitis pol 1ab (1082)	-----	LVLPSEVVKGLQCVNNVVGPRHGDNN	HE		
bovine coronavirus pol 1ab (1374)	RVYKHLNKYDCVVTTELTSAGTESVPS	DVSLTYLLGTAEK			
Human corona 229E pol 1ab (1185)	VSEVVKPVCSSTIFRGAVSCSHYQIN	ISONLCVDGFGVN			
Murine hepatitis pol 1ab (1421)	RAYOHINKCDNVVTLTTSAGTESVET	DVSLTYLLGCVTK			
Consensus (1444)	RAY HINKCD VVTTLISAGIFSVPS	DVSLTYLLG L K			
Section 39					
	(1483)	1483	1490	1500	1510 1521
avian infectious bronchitis pol 1ab (1110)	KLVAAYKNVLVDGVNNYVVPVLSLGI	FGVDFKMSIDAMR			
bovine coronavirus pol 1ab (1413)	QVVLVSNNQDEDFDLISKQITAVEG	TKKLAERLSFNVGR			
Human corona 229E pol 1ab (1224)	ETQPTWN-----DALNT	CIKDADYNARVELSVTPIK			
Murine hepatitis pol 1ab (1460)	NVTHIVSNNQDDFDVTERCOVTSV	AGTKASLQIAKNICR			
Consensus (1483)	KVVLVSNNQDDFDVIAKCQITLVDG	TKALALKLSINLIR			
Section 40					
	(1522)	1522	1530	1540	1550 1560
avian infectious bronchitis pol 1ab (1149)	EAFEGCTIRVLLFS	-----	-----	-----	-----
bovine coronavirus pol 1ab (1452)	STVYETDANKLILSNDVAEVSTENV	LQDVLSLRHDI	ALD		
Human corona 229E pol 1ab (1256)	NTVDTTPKEEFVVKENLNAFLV	HDNVAFYQGDVDTMVNC			
Murine hepatitis pol 1ab (1499)	DVKFVTNACSSLES-ESCEVSS	YDVLQDFEALRHDI	OLD		
Consensus (1522)	DIVF T A LLFS DL FVSSH	DVLQDV ALRHDI LD			
Section 41					
	(1561)	1561	1570	1580	1599
avian infectious bronchitis pol 1ab (1163)	-----	-----	-----	-----	-----
bovine coronavirus pol 1ab (1491)	DDARTEFVQSNVDVMP	EGWRVYNKEFYQINGV	RTVKYEECP		
Human corona 229E pol 1ab (1295)	VDFDFLVNAANENLAHGGG	AKALDVYTKGKLQRLSKEH			
Murine hepatitis pol 1ab (1537)	DDARVEVQANMDC	LPTWRFLVNKFDSDV	GVRTIKYEECP		
Consensus (1561)	DDAR FVQANMD LP GWRLVN	KFD I GVRTIKYEECP			
Section 42					
	(1600)	1600	1610	1620	1638
avian infectious bronchitis pol 1ab (1163)	--LSQEHID--	-----	-----	YFD--VTCKOKTLEY	
bovine coronavirus pol 1ab (1530)	GGTILICSQDKVFCYVOQGS	ENKATVAQIKALFTDKVDIT			
Human corona 229E pol 1ab (1334)	IGLAG-----	KVKVGTGVMVECD	SIRIFNVV		
Murine hepatitis pol 1ab (1576)	GGIFVSSQCKKEGYVQNGS	FKASVSOTRALLANKVDVL			
Consensus (1600)	GGIAI SQDK FGYVQNGS	FK ATVAQIKALS	LLKKVDIL		

21/199

FIGURE 4A (contd.)

Section 43						
	(1639)	1639	1650	1660	1677	
avian infectious bronchitis pol 1ab (1182)		LTREDGVKYSIVLKP	GDSLGQFG	-----	QVYAKN	
bovine coronavirus pol 1ab (1569)		LTVDGVNFTNREVPV	GESFGKSLGNV	EC	DGVNVTKHRC	
Human corona 229E pol 1ab (1360)		GPRKCKNERDILLKAYN	RIINNEQGTPTLPTIT	SCGIFG	GIK	
Murine hepatitis pol 1ab (1615)		CTVDGVNFRS	CCYAECEVEGKTL	GSVECDG	INVTKVRC	
Consensus (1639)		LTVDGVNFRSILVK	GESFGKSLGSV	FC	DGINVTKHKC	
Section 44						
	(1678)	1678	1690	1700	1716	
avian infectious bronchitis pol 1ab (1211)		KIVFTADDVEDKE	ILYVPTTDKS	ILEYMG	LDAQKYVIYL	
bovine coronavirus pol 1ab (1608)		INAKGKVEEQEDNLS	SEDLKAVRSEN	DQKEL	LAYYNNM	
Human corona 229E pol 1ab (1399)		LETSLEMLLDVCNTR	KVRMFVYTDTEVCKV	KDFVS	GLVN	
Murine hepatitis pol 1ab (1654)		ATYKGVSEFQVSD	SEADLVAVKDA	EGDEP	OTLKYATM	
Consensus (1678)		IIYKGVFFQF	NLSEVDL	AVSDSF	FDKDLLAYY M	
Section 45						
	(1717)	1717	1730	1740	1755	
avian infectious bronchitis pol 1ab (1250)		QTLAQKWNVOYRDNEL	ILEWRDGNCGWISS	SAIVL	BOAAKT	
bovine coronavirus pol 1ab (1647)		LVNCSKRWQVVEG	KYETEKQANNNG	FNVSCL	MLQSLNH	
Human corona 229E pol 1ab (1438)		VQKVEQPKTEPK	-PVSVIKVAPKPYR	MDGKFSY	ETEDLL	
Murine hepatitis pol 1ab (1693)		LG-MCKW	SVVCGNYFAIK	OSNNNGY	INVACLMLQHTST	
Consensus (1717)		L M KWNV	VFKGN	YFIFKQANN	NCFINVACLMLQAL L	
Section 46						
	(1756)	1756	1770	1780	1794	
avian infectious bronchitis pol 1ab (1289)		REKGE	LTEAWAKLLG	-GDPTDEVAWCY	SCTAKVGDFSD	
bovine coronavirus pol 1ab (1686)		KEKIVQWQEAWLE	FRSGRPAREVSLVL	KGGFKEG	DEPA	
Human corona 229E pol 1ab (1476)		CVADDKPIVLE	TESMLTLDDRGL	ALDN	LSQVLSAAIK	
Murine hepatitis pol 1ab (1731)		KEPKWQWQEAWNE	FRSGKPLREVSLVL	KGSEKENE	PS	
Consensus (1756)		KFK EQWQEAW	EFRSGK	REVALVLAK	GGFKEGDPSD	
Section 47						
	(1795)	1795	1800	1810	1820	1833
avian infectious bronchitis pol 1ab (1327)		ANWLIANTAEHFD	ADYTNAFLK	KRVSN	CGIKS	-----
bovine coronavirus pol 1ab (1725)		SRDFLRVV	VFSQVDLTGA	ICDFEL	CKGVKQE	EORTGVDA
Human corona 229E pol 1ab (1515)		QVDINKATP	-SGMLIKFD	IGSVVVM	VVPSE	--KDKHL
Murine hepatitis pol 1ab (1770)		SIDIMRV	VLRADLSGAT	ONLEFVCK	GVKQE	QRKGVDA
Consensus (1795)		SIDFLRVV	ADLSGA	C LEIVCK	CGVKQE	QRKGVDA
Section 48						
	(1834)	1834	1840	1850	1860	1872
avian infectious bronchitis pol 1ab (1360)		--YELRG	----	LEACIQPVR	ATNLLHF	KTOYSNCPETCGA
bovine coronavirus pol 1ab (1764)		VMHFGT	LSREDLEIGY	TVDCSCG	KKLHCVR	EDVPFLIC
Human corona 229E pol 1ab (1551)		DNNVQR	CTRKLNR	LMCDIVCT	IPADY	LPVLSSLTCNV
Murine hepatitis pol 1ab (1809)		VMHFGT	LLKGD	EVRCYNTACT	CGSKLVHCT	QENVPFILIC
Consensus (1834)		VMHFGT	LSR DLEIGY	NIVCTCGAK	LIHCL	FNVPFLIC

22/199

FIGURE 4A (contd.)

Section 49						
	(1873)	1873	1880	1890	1900	1911
avian infectious bronchitis pol 1ab (1393)	NN	TD	EVIEASLPYELL	FATD	GPATV	CCDEDAVGTVVFMG
bovine coronavirus pol 1ab (1803)	SNT	PAS	MKLRKGVGS	ANIFK	GDKVGHVHV	KCEQSYQLY
Human corona 229E pol 1ab (1590)	SFV	GEL	KAAEAKVLT	IKVTE	DGVNMH	DVTVTITDKSEEQ
Murine hepatitis pol 1ab (1848)	SNT	PEGR	KLEDDVVA	ANFTT	GGSVGHYTHV	KCKPKYQLY
Consensus (1873)	SNT	PELR	KLKP	VISANIT	DGGAVVHYVHV	KCD SYQLY
Section 50						
	(1912)	1912	1920	1930	1940	1950
avian infectious bronchitis pol 1ab (1432)	STNS	GHCYT	CAAG	QAFDN	LAKDR	KFGKKSPYITAMYTRE
bovine coronavirus pol 1ab (1842)	DASN	VKKVTD	VTEN	ESDGL	YLKNE	KOTERSVLTTYYLDD
Human corona 229E pol 1ab (1629)	VGVI	ADKDK	DLSS	AMP	SDINT	SELTKAIDVDWVEFYGE
Murine hepatitis pol 1ab (1887)	DACN	VNKVSE	DAFEN	TDC	YLKNE	KOTESSVLTTYYLDD
Consensus (1912)	DA	NV	KVTD	ASGNL	SDCLYL	KNLKQTESSVLTTYYLDF
Section 51						
	(1951)	1951	1960	1970	1980	1989
avian infectious bronchitis pol 1ab (1471)	AFK	NET	SLP	AKQSK	GKSKSV	KEDVSNLATSSKASF
bovine coronavirus pol 1ab (1881)	VKK	LEY	NED	LSQYY	CDGCK	YYTQRITKAQFKTEFKVDGV
Human corona 229E pol 1ab (1668)	KDA	MT	ATV	DHSA	EAYESA	VVNGIRVLKTS
Murine hepatitis pol 1ab (1926)	VKC	VEY	PDI	LSQYY	CDGCK	YYTKPILKAQFKTEFKVDGV
Consensus (1951)	VKK	VEY	APD	LSQYY	CD SKYYT	I IKAQFKTEFKVDGV
Section 52						
	(1990)	1990	2000	2010	2028	
avian infectious bronchitis pol 1ab (1510)	TDEE	QWY	DSNI	YESL	KVQES	PDNFDKYV
bovine coronavirus pol 1ab (1920)	YTNE	KL	LIGHT	ICDI	LNAK	LGFDSSKEE
Human corona 229E pol 1ab (1707)	CIAL	QYSK	PHFIS	QGLD	AAWN	KFVLGD
Murine hepatitis pol 1ab (1965)	YTNE	KLV	SHS	IAEK	LNAK	LGHDCNSPE
Consensus (1990)	YTNE	FQ	LIGH	SI E	LNAK	LGFD FVEYKVT
Section 53						
	(2029)	2029	2040	2050	2067	
avian infectious bronchitis pol 1ab (1549)	LTE	KVRC	IKSV	DFRS	KGGFI	MYKLTPD
bovine coronavirus pol 1ab (1959)	GDV	V	LAT	DDLY	VKRYE	RGCITFGK
Human corona 229E pol 1ab (1746)	RLM	KG	DCDA	EDTL	TKLS	KYLANEAQ
Murine hepatitis pol 1ab (2004)	GDV	V	L	ASDD	LYVS	RYSSG
Consensus (2029)	GDV	V	L	ASDD	LYVS	RYSSG
Section 54						
	(2068)	2068	2080	2090	2106	
avian infectious bronchitis pol 1ab (1588)	VLD	AIS	IKAT	WVEGN	ANFV	GHFNYY
bovine coronavirus pol 1ab (1998)	TYF	NR	PL	LDEN	KF	DKVDDVD
Human corona 229E pol 1ab (1785)	AK	E	NSV	AS	ENSA	IVCAS
Murine hepatitis pol 1ab (2043)	TYF	NR	PS	V	CEN	KFNVL
Consensus (2068)	TYF	NR	SL	L	V	IENKFNVL

FIGURE 4A (contd.)

Section 55									
	(2107)	2107	2120	2130	2145				
avian infectious bronchitis pol 1ab (1615)		-----			-----KSLHI				
bovine coronavirus pol 1ab (2024)		-----			-----DISESDAKES				
Human corona 229E pol 1ab (1812)		-----			-----YCVHC				
Murine hepatitis pol 1ab (2082)		PGADASAGAGIAKEQKACASASVEDQVVT			EMRQEPSVSA				
Consensus (2107)				DI	SVHA				
Section 56									
	(2146)	2146	2160	2170	2184				
avian infectious bronchitis pol 1ab (1620)		PTFWENAENFVKMGDKIGGVIMGLWRASHLNKPNLERTF							
bovine coronavirus pol 1ab (2034)		KEINIEKTSGVKKKFKVEDSVLVNDDTSEIKYVKSLSTV							
Human corona 229E pol 1ab (1817)		--IKYYSRVRSVRGRADIVSMEQLEPCAOSRLLESQVAYT							
Murine hepatitis pol 1ab (2121)		ADVKEVKLNGVKKPKVKEGSAVNDPTSETKMKVKSLSIV							
Consensus (2146)		DIKEIKLNGVKKP	KIEGSAVINDPTSESKLVKSLSIV						
Section 57									
	(2185)	2185	2190	2200	2210	2223			
avian infectious bronchitis pol 1ab (1659)		NTAKKAIVSSVTTQCGKLIGKAATFIADKMGGGVMRN							
bovine coronavirus pol 1ab (2073)		DVYDMWLTGCRYVVRTANALSMANVPTERRKFKKFGMTL							
Human corona 229E pol 1ab (1854)		AFSGPVDKGHYTYDTAKKSMYDGDREVKHDLSSLSTTS							
Murine hepatitis pol 1ab (2160)		DVYDMFLTCKYVWTANELSRLVNSPTREYMKWKGK							
Consensus (2185)		DVYDMFLTGCCKYVV	TANKLS	VNSPTIRKVIKFGVT					
Section 58									
	(2224)	2224	2230	2240	2250	2262			
avian infectious bronchitis pol 1ab (1698)		ITDSLKGECGITRG-----				-----HFER			
bovine coronavirus pol 1ab (2112)		VSLPDELNLREIKPVENVVKAVERNKISACFNFKKWTLM							
Human corona 229E pol 1ab (1893)		VVMVGGYMAPVNTVKPKPMENQDDEKAQKFEDEGDELTH							
Murine hepatitis pol 1ab (2199)		IVTFAKLLLRDEKQEVAPKVVAKAIAICYCAVKNFLI							
Consensus (2224)		IVIPIKLLLRD	K	F	VIK	VK	KA	ACF	FIKWLIL
Section 59									
	(2263)	2263	2270	2280	2290	2301			
avian infectious bronchitis pol 1ab (1716)		KMSPOFLKTLMEFFDFYFLKAS-----				-----VKS-----V			
bovine coronavirus pol 1ab (2151)		LLFGWTKISADNKVIYTTTEVASKLTCKLVALAEKNAFLT							
Human corona 229E pol 1ab (1932)		NEVIEFTWLESMTTECKTAVTGGDVKIMAKAPORTGVVL							
Murine hepatitis pol 1ab (2238)		YCESWIKENTDNKVIYTTTEVASKLTFRCCIAFKNALQT							
Consensus (2263)		LF	WIKFSLDNKVIYTTTEVASKLT	KL	LAFKNALLT				
Section 60									
	(2302)	2302	2310	2320	2330	2340			
avian infectious bronchitis pol 1ab (1741)		VASYKEVLCKVVLATLLIVFEVYTSNPVMTGIRVLDFL							
bovine coronavirus pol 1ab (2190)		EKWSVARGACTEATIELLINFNIYANVIFSDFYLPKIG							
Human corona 229E pol 1ab (1971)		KRSLKYNLKASAAVLKSKWLLAKETKLLLLIMTLYSVV							
Murine hepatitis pol 1ab (2277)		ENWSVSRGFFELVATVELLINFNIYANVILSDFYLPNIG							
Consensus (2302)		EKWSVARGA	IIATIFLLWFNFIYANVILSDFYLP	IG					

24/199

FIGURE 4A (contd.)

					Section 61
	(2341)	2341	2350	2360	2379
avian infectious bronchitis pol 1ab (1780)		REGSLCCPYKDYG	-----	-----	KDSFDVLRVCA
bovine coronavirus pol 1ab (2229)		FLPTEVCKEAOIMKSTFSLVTICDLYSTCDVGEKNOYON			
Human corona 229E pol 1ab (2010)		LLCVRF-----PEN-----FCSETVN--GYAKSNEVKDDYCD			
Murine hepatitis pol 1ab (2316)		PLPTEVQOTVAFKTTTEGVSTICDFYQVTDLGYRSSECN			
Consensus (2341)		FLPTEVGIW KSTFL TICDY IKDLGEK YCN			
					Section 62
	(2380)	2380	2390	2400	2418
avian infectious bronchitis pol 1ab (1804)		DDETCRVGLHDKDSARLYKHAYSNEQVYKDAASGFIENW			
bovine coronavirus pol 1ab (2268)		GSLAOFCLAGEDMDNYKATDVWQYHEDRRAFVDYTGW			
Human corona 229E pol 1ab (2041)		GSLGCKMCLFGYOELSOEHLIDVWVKHETDPLFSNMQPF			
Murine hepatitis pol 1ab (2355)		GSMVCELCFSGEDMDNYDAINVMQHVVDRRLSFDYISL			
Consensus (2380)		GSIIICKLCLAGFDMDNYKHIDVVQHVDRRLS DY V			
					Section 63
	(2419)	2419	2430	2440	2457
avian infectious bronchitis pol 1ab (1843)		NWLYEVEFLLEVKPVAG-----FVH--TCYCVKYLVLN			
bovine coronavirus pol 1ab (2307)		KKRVGEELIMSYALTAWYKPLAESHQSLTWLPELFM			
Human corona 229E pol 1ab (2080)		LVNVLLHIFG-----DNYTRCFLLYEVAQMIS			
Murine hepatitis pol 1ab (2394)		FKLVVETVEGYSLYTVCFYPLEVLLIGNOLLTWLPELFM			
Consensus (2419)		IKLVLELIIGYALYTA FYPLF LIIIQILTTWLPELFM			
					Section 64
	(2458)	2458	2470	2480	2496
avian infectious bronchitis pol 1ab (1874)		STVLQTVGCFEDMEVQTMFSHFNMGAGFYFWETFKYYT			
bovine coronavirus pol 1ab (2346)		LSTLHWSVRLLEWLANMLPAHVEMRFYITIASFKLFIIL			
Human corona 229E pol 1ab (2107)		TVGMFLGYKETNWEHLHFIHFDVICDELELVIVIVKVISF			
Murine hepatitis pol 1ab (2433)		LETMHSARLFEVAVNMRFETLEREYVVTAMYKVYCL			
Consensus (2458)		LSTLHWSVRLLEWLANMLPAHVILRFYIVI ALIKVI L			
					Section 65
	(2497)	2497	2510	2520	2535
avian infectious bronchitis pol 1ab (1913)		QVAHLLYCKDVTCEVCKRVARSNRQEMSVVVGGRKQIVH			
bovine coronavirus pol 1ab (2385)		FRHVAAGCSKPGCLFCYKRNRSRLRVKCSITIGCMIRYYD			
Human corona 229E pol 1ab (2146)		VRIVLEGUENDDCTACSKSARLKRFEMTILNGVQRSEY			
Murine hepatitis pol 1ab (2472)		CRHVMYGCSPGCLFCYKRNRSRLRVKCSITIGCMIRYYD			
Consensus (2497)		RHVIYGCSPGCLFCYKRNRSRLRVKSTIVGGMIRYYD			
					Section 66
	(2536)	2536	2550	2560	2574
avian infectious bronchitis pol 1ab (1952)		MYTNSCYNECKRNWYCRNCDDYGHQNGFMSPFVAGEIS			
bovine coronavirus pol 1ab (2424)		VMANGGTGFCCKHOWNCDDSYKPGNTFITVEAADLS			
Human corona 229E pol 1ab (2185)		VMANGGSKCKKREFAVDSDSYGYGSCFITVVSREIG			
Murine hepatitis pol 1ab (2511)		VMANGGTGFCCKHOWNCDDSYKPGNTFITVEAADLS			
Consensus (2536)		VMANGGTGFCCKHOWNCDDSYKPGNTFITVEAADLS			

FIGURE 4A (contd.)

Section 67					
	(2575)	2575	2580	2590	2600 2613
avian infectious bronchitis pol 1ab (1991)	EKLKRHV	PTAYACHV	DEACLV	DEVN	KYKAATPGKD
bovine coronavirus pol 1ab (2463)	KELKRPIQ	LDVAIHT	VTDVKQ	GCYMR	EYERDGGORTX
Human corona 229E pol 1ab (2224)	NIT	TNVQPT	CPPEVM	DKVEFENG	EYRLVSCETFWRYN
Murine hepatitis pol 1ab (2550)	KELKRPNV	PTDSN	YSVTEVKQ	VGCSMRL	EYERDGGORVY
Consensus (2575)	KELKR	PVQPTD	AYHTV	TEVKQV	GCFMRLFYERDGGOR Y
Section 68					
	(2614)	2614	2620	2630	2640 2652
avian infectious bronchitis pol 1ab (2030)	SASSAVKCF	SVTDEL	KKAVFLKEA	CKCEQ	ISNDGFIVCN
bovine coronavirus pol 1ab (2502)	DDVNASL	FVDYSN	LLHSKVKG	VPMHVVVV	END-----
Human corona 229E pol 1ab (2263)	FDTTESKY	SCKEVFKH	---CNVLD	DFLMFNN	MG-----
Murine hepatitis pol 1ab (2589)	DDVNASL	FVDMGL	LLHSKVKG	VPEHVVVV	END-----
Consensus (2614)	DDVNASL	FVDMS	LLHSKVKG	VPDLHVVVV	END
Section 69					
	(2653)	2653	2660	2670	2680 2691
avian infectious bronchitis pol 1ab (2069)	TQSAHALE	CAKN	ATLYAGY	CKKELID	DOAYEQLVVE
bovine coronavirus pol 1ab (2535)	---	ADKANFLN	AAVEYAQ	SLFRILM	VDKNLTITANTG
Human corona 229E pol 1ab (2293)	---	TNVTQVKN	SVYES	LICRILK	IVDSELTSLSMV
Murine hepatitis pol 1ab (2622)	---	ADKACEL	CAVELA	SYRPM	MMVEKKLTITANTG
Consensus (2653)	---	ADKANFLN	AAVFYAQ	SLCRPIL	MVDKLTITLNVG
Section 70					
	(2692)	2692	2700	2710	2720 2730
avian infectious bronchitis pol 1ab (2108)	PVS	-KSVI	DKVCS	LISS	LISSVTAAIN-----
bovine coronavirus pol 1ab (2570)	T	SVT	ETMEDV	VYVDT	ETLSMEDVKKSLNAL
Human corona 229E pol 1ab (2328)	FNG	---	VLDKAY	IDVLRN	SEKDLN-----AN-----
Murine hepatitis pol 1ab (2657)	L	SVSR	ETMEDL	YVDS	ELNVLDVPEK
Consensus (2692)	SVSK	ETMEDL	YVDTLLS	IFDV	DKKSLNA IAH SIK
Section 71					
	(2731)	2731	2740	2750	2769
avian infectious bronchitis pol 1ab (2134)	---	---	YKAGTL	RDALLS	ITKDEBAVDMAIFCHN
bovine coronavirus pol 1ab (2609)	G	TOTCKV	EDTE	ESCAK	KCSIDSDVDTKCLADSVMSAVS
Human corona 229E pol 1ab (2352)	---	---	MSLA	CKRAL	GLSLSDMETSAISNAHR
Murine hepatitis pol 1ab (2696)	G	VOLEQ	YMDTE	TCARRK	CAIDSDVETK
Consensus (2731)	G	QI	VLD	TFISCARKK	CAIDSDVDTREITDSVMSAVN
Section 72					
	(2770)	2770	2780	2790	2808
avian infectious bronchitis pol 1ab (2162)	H	VDYT	CDG	ETNV	LPSYGIDTGKLP
bovine coronavirus pol 1ab (2648)	A	GLE	ITDES	CNNLV	PTIRG-DNIVAA
Human corona 229E pol 1ab (2380)	C	DVLES	DLSEN	IFVSS	AKPEEKESAY
Murine hepatitis pol 1ab (2735)	A	GVD	ETDES	CNNLV	PTVKS-DTEVAAD
Consensus (2770)	AGV	DLTDES	FNNLV	PSYK	DKIVAADLGVLIQN AKH

FIGURE 4A (contd.)

Section 73						
	(2809)	2809	2820	2830	2847	
avian infectious bronchitis pol 1ab (2201)		ANLRMKNAP--	EVVAKFSELIRL	DSCLKYLISATVKS		
bovine coronavirus pol 1ab (2686)		VOGNVAKIACV	SVDAFNQ	SDFOHKLKACCKTG		
Human corona 229E pol 1ab (2419)		VNANVLTIKDQ	TRIMAHKDENSE	SAEGRKYIMKTSKAKG		
Murine hepatitis pol 1ab (2773)		VOANVAKAANVACI	SVDAFNQ	SADLOHRLKACSKTG		
Consensus (2809)		VNANVAKAANVPC	IWSVDAFNQLSAD	QKYLRKAC	KTG	
Section 74						
	(2848)	2848	2860	2870	2886	
avian infectious bronchitis pol 1ab (2238)		VREFITKSGAKQ	VIACHTOKLLVEKKAG	GIVSGTFKCEK		
bovine coronavirus pol 1ab (2725)		LKLLKITYNKQ--	MANVGLTTPESLKG	GAVER		
Human corona 229E pol 1ab (2458)		LTLLLTINEMQAV	TOIPATSIIVAKQGA	DAGH		
Murine hepatitis pol 1ab (2812)		LKLLKITYNKQ--	EANVPILTTTPESLKG	GAVER		
Consensus (2848)		LKFKLTYNKQ	VANVPILTTTPESLKG	GAVER		
Section 75						
	(2887)	2887	2900	2910	2925	
avian infectious bronchitis pol 1ab (2277)		SYFKWLLT	YILLETACCSGY	YYMEMSKS	FVHPMYDVNST	
bovine coronavirus pol 1ab (2755)		-----YFVY	VCELLSLVCF	FIGEWCLEMT	TVHKSDFO	
Human corona 229E pol 1ab (2490)		-----SLFW	LLCGIVCLIQ	YLCFFMPYFMY	DIVSS	
Murine hepatitis pol 1ab (2842)		-----RMLQ	WLEVANTICE	IVLRLMPTVAVHKS	DMOL	
Consensus (2887)			ILYILFLA	LVCFT	LWLLMPTYHVMYSDMS	
Section 76						
	(2926)	2926	2940	2950	2964	
avian infectious bronchitis pol 1ab (2316)		LHVEGEHVIDKGV	LRDIVPDT	CFSKVNDAFWGRPY		
bovine coronavirus pol 1ab (2788)		PVYASYRVLDN	VLRDVSVEDV	CFANKFOQDQWYESTE		
Human corona 229E pol 1ab (2523)		PEGYDFYENQ	QKNEFLAPLKVR	IVNENEDWHYAKE		
Murine hepatitis pol 1ab (2875)		PLYASEVIDN	VLRDVSVD	CFANKFOQDQWYESTE		
Consensus (2926)		PLYASEKVIDNGV	LRDVSVED	CFANKFENFDQWYESTE		
Section 77						
	(2965)	2965	2970	2980	2990	3003
avian infectious bronchitis pol 1ab (2355)		DNSRNCPIV	TAVIDGDGT	VATGVPGEVSWV	MDGVMFTHM	
bovine coronavirus pol 1ab (2827)		GLSYYSNSMA	----	CPIVVAVVDQ	DLGSTVFNVP	TKVLR
Human corona 229E pol 1ab (2562)		GTPLNK-Q	----	SCPIVVGVS	ELVNTVA	IPSNVYL
Murine hepatitis pol 1ab (2914)		GLAYYRNSKA	----	CPVVVAVIDQ	DIGHTLENVPT	VLR
Consensus (2965)		GLSYYNSMA		CPIVVAVGVQ	DIVSTVFNVPT	VLR
Section 78						
	(3004)	3004	3010	3020	3030	3042
avian infectious bronchitis pol 1ab (2394)		TQTERKPPWYI	PTWFNREIVG	YTQDSIT	TEGSEYTSIALF	
bovine coronavirus pol 1ab (2862)		YGYHVLHFI	THAFADGVQ	CYTPHSQTS	MSNEYASGCVL	
Human corona 229E pol 1ab (2594)		VGKTLTFTLQ	AAPNAGVCYD	IEGVTTPEK	-----GTF	
Murine hepatitis pol 1ab (2949)		YGEHVLHFI	THAFADSVOCY	TPHMOIPYD	NFYASGCVL	
Consensus (3004)		YGFHVLHFI	THAFANDGVQ	CYTPHSQIPY	NFYASGCVL	

27/199

FIGURE 4A (contd.)

Section 79					
	(3043)	3043	3050	3060	3070 3081
avian infectious bronchitis pol 1ab (2433)		SARCLYETASNTTPOLYCFNGDNDAPSEALPEG	ITIPHRVY		
bovine coronavirus pol 1ab (2901)		SSACTMAMADGSPOPYCYTEGLMGNASLYS	EVPHVR		
Human corona 229E pol 1ab (2627)		TSACTRLEGLGGN-NVYCYNTALMEGSLPYSSIQANAYS			
Murine hepatitis pol 1ab (2988)		SSLCTMLAHADGEPHRYCYTCGVMHNASLYSCLAPHVR			
Consensus (3043)		SSACTMLAAADGSPNPYCYTDGLM	NASPYSSIIPHVR		
Section 80					
	(3082)	3082	3090	3100	3110 3120
avian infectious bronchitis pol 1ab (2472)		FQPNG--VRLIVPQQLHTPYV	KFVSDSYGEGSVCEYT		
bovine coronavirus pol 1ab (2940)		NEANAKGFIRPEVIREGLIVRTVTRSMSCYCRVGLCEEA			
Human corona 229E pol 1ab (2665)		KYDNGNFIKLPVEAOGFGFRTRTIATKPSVGEVVE			
Murine hepatitis pol 1ab (3027)		NLAQNGYIRPEVWSEGLVRVTRSMTCYCRVGLCEEA			
Consensus (3082)		NLANGNGVIRFPEVL	EGIVRVVTRSMSCYCRVGLCEEA		
Section 81					
	(3121)	3121	3130	3140	3159
avian infectious bronchitis pol 1ab (2509)		RPSYGVSLNPQWLFNDENTSKPEV	GSTVREIMFIMV		
bovine coronavirus pol 1ab (2979)		DEICFENENGSWLNNDYRSHPCTEGARDVFDIYQLE			
Human corona 229E pol 1ab (2704)		NAGVDEGDKWENUG--RVANGYVETGLWNVENH			
Murine hepatitis pol 1ab (3066)		EEICFENENRSWLNNPXYRAMPTEGRNAEDTHOV			
Consensus (3121)		DEGICFENKSWVLNNDYRSLPGTFCCR	VFDLIFQIL		
Section 82					
	(3160)	3160	3170	3180	3198
avian infectious bronchitis pol 1ab (2548)		STFEFGVNPNTYMOLATMPETLVVVVLTAMVINEQGV			
bovine coronavirus pol 1ab (3018)		KGLAOPVDFELALTASSIAGAILAVIVVLIFYLLIKLRA			
Human corona 229E pol 1ab (2740)		SMESSEFSVAAMSGCILLNCAIGAFATCCCELVTFRM			
Murine hepatitis pol 1ab (3105)		GGLVRPTDEFALTASSVAGAILATIVVLAIFYLLIKLRA			
Consensus (3160)		SGLASPVD	ALTASSIAGAILAVIVVLIFYLLIKLRA		
Section 83					
	(3199)	3199	3210	3220	3237
avian infectious bronchitis pol 1ab (2586)		KAYARTPTMTIVVVTIAFLICWHSYNSVLAVILLVLY			
bovine coronavirus pol 1ab (3057)		GDYTSIEVNVIWCVFMMLEFQVYPTLSCVYATCY			
Human corona 229E pol 1ab (2779)		GDLSVGCTVVVAVLENNVSYINTONLVMTIAYAILYE			
Murine hepatitis pol 1ab (3144)		GDYTSIVVNVIWGLFLMLLEFQVYPTLSCVYACEY			
Consensus (3199)		FGDYTSIVFINVIWVCINFLMLFVQVYPTLSCIYAFY			
Section 84					
	(3238)	3238	3250	3260	3276
avian infectious bronchitis pol 1ab (2625)		CYASTVTRNTVIMHCWLVFTEGLIVPTLACCYLGFL			
bovine coronavirus pol 1ab (3096)		FYATLYPSEISVIMHLOWLVMYGTIMLFCLLISVV			
Human corona 229E pol 1ab (2818)		FATRSRLR--YA-WIWCAAYLIAYISFAWLCAWFLAM			
Murine hepatitis pol 1ab (3183)		FYTTLYFPSEISVIMHLOWLVMYGATIMLFCILVAVV			
Consensus (3238)		FYTTLYFPSEISVIMHLOWLVMYGSIMPLWLCIIYIAVV			

28/199

FIGURE 4A (contd.)

Section 85				
	(3277)	3277	3290	3300 3315
avian infectious bronchitis pol 1ab (2664)		NYMYTPLFLWCYGTTRKNTKRYDGNFVGNVYDLAAKS		
bovine coronavirus pol 1ab (3135)	VS	-----NHAFWVFAYGRREGTCVRSDDTEEMALTTT		
Human corona 229E pol 1ab (2854)	LTGL	----LPSSLKLVSTNIFEGDKFVTFESAAGTF		
Murine hepatitis pol 1ab (3222)	VS	-----NHALWLFYCRKLGTVRSVGTFEEMALTTT		
Consensus (3277)	VS		NHALWLFKYCRKLGTVRSVGTFEEMALTTT	
Section 86				
	(3316)	3316	3330 3340	3354
avian infectious bronchitis pol 1ab (2703)		VIRGSEFVMTNEEG-DKFEAYLSAYARLKYYSGTGSEQ		
bovine coronavirus pol 1ab (3168)		MITKDSYCKLKNSISDVAENRYLSLNKYRYSEKMDTA		
Human corona 229E pol 1ab (2889)		VDMRSYERANSTISPEKLSAASNRKYRYGNANEA		
Murine hepatitis pol 1ab (3255)		MITKESYCKLKNSISDVAENRYLSLNKYRESEKMDTA		
Consensus (3316)		MITKDSYCKLKNSISDVKFNRYLSLYNKYKYSGKMDTA		
Section 87				
	(3355)	3355	3360 3370 3380	3393
avian infectious bronchitis pol 1ab (2741)		DRLQCRAWLYLDQYR-NSGVEIVTIRYISIGVRI		
bovine coronavirus pol 1ab (3207)		AIREACSQLAKAMDTFTNNNGSDVLYQPTASVSTFT		
Human corona 229E pol 1ab (2928)		DRCGYAYLAKMLDESROHN-DIDTITVSYG-STL		
Murine hepatitis pol 1ab (3294)		AIREACSQLAKAMETENHNNNGNDVLYQPTAVTTSFL		
Consensus (3355)		DYREACCAQLAKAMDTFSNNGDILYTPPTASVGTSFL		
Section 88				
	(3394)	3394	3400 3410 3420	3432
avian infectious bronchitis pol 1ab (2779)		QSGFKLVSPSSAVKLEYSVSRGNMIGINIGITF		
bovine coronavirus pol 1ab (3246)		QSGIVMVSITSKPITSVTGNMTLNLGLDKVYC		
Human corona 229E pol 1ab (2965)		QACLRMAOTSGFKQVRCGNTVENLWLGIV		
Murine hepatitis pol 1ab (3333)		QSGIVMVSITSKPITSVTGNMTLNLGLDKVYC		
Consensus (3394)		QSGIVKMVSPSSKVEFCIVSVTYGNMTLNLGLWLGDKVYC		
Section 89				
	(3433)	3433	3440 3450 3460	3471
avian infectious bronchitis pol 1ab (2818)		PRHVLGKFSGDQWNEVLNLIANNHEFEVTTQHG--VTIN		
bovine coronavirus pol 1ab (3285)		PRHVICASADMTNPYTNLLCRVTSSDFTVLFRLSLT		
Human corona 229E pol 1ab (3004)		PRHVIASN-TTSAIPYDHEYSIMRLHNESTISGTAFGV		
Murine hepatitis pol 1ab (3372)		PRHVICSSADMTDPPXPNTLCRVTSSEFCVMSGRMSLT		
Consensus (3433)		PRHVICSASDMT PDY NLLCRVTSSDFTVISGRLSLTV		
Section 90				
	(3472)	3472	3480 3490 3500	3510
avian infectious bronchitis pol 1ab (2855)		VSRRDKAVLLIQTAVANAEEKKYKIKANCDSETTAC		
bovine coronavirus pol 1ab (3324)		MSYQMQGCMVLTVTLQNSRTPKYTGCVVKPGETTVLA		
Human corona 229E pol 1ab (3042)		VCATMNEVTKEIVSQTMHERRHSRTLKSEGENILA		
Murine hepatitis pol 1ab (3411)		MSYQMQGCMVLTVTLQNTNTKYSQGVVKPGETTVLA		
Consensus (3472)		MSYQMQGCMVLTVTLQNA TPKYSPGVVKPGETFTILA		

29/199

FIGURE 4A (contd.)

Section 91					
	(3511)	3511	3520	3530	3549
avian infectious bronchitis pol 1ab (2894)		AACGIVVGLYPTMP	SNCTIRASTLAGACG	SVCFNIEKG	
bovine coronavirus pol 1ab (3363)		ATNGKPOGAFHV	TMRSSYTLKGSFLCGS	ICSVGYVLMGD	
Human corona 229E pol 1ab (3081)		CYDGCAGQVEFV	GNMTNNWTTTSGS	TINGACGPSYNLKNG	
Murine hepatitis pol 1ab (3450)		AYNGRPQGAFTHT	LTSSHTLIKGSFLCGS	ICGVVYVLTGD	
Consensus (3511)		AYNGKPOGAFHV	TMRSSWTIKGSFLCGACG	SVGYVL GG	
Section 92					
	(3550)	3550	3560	3570	3588
avian infectious bronchitis pol 1ab (2933)		VVNFFVMHHL	LPNALHTGTDLM	EEFYGGVDEEVAQRV	
bovine coronavirus pol 1ab (3402)		CVKVVYHQHLE	STGCHTGTDFENODF	CPYKDAQVVCLE	
Human corona 229E pol 1ab (3120)		EVEFVYHQHLE	SGSGSHVGSSEDEVM	FGHEHQPNIDVE	
Murine hepatitis pol 1ab (3489)		SNRVVMHQHLE	STGCHTGTDESNEY	GBYRAQVVCLE	
Consensus (3550)		VKEFVMHQLEL	STGCHTGTDF GDFYGPYKDAQVVCLE		
Section 93					
	(3589)	3589	3600	3610	3627
avian infectious bronchitis pol 1ab (2972)		PPDNIVNNI	VAWFAHLSVKESSFSLPKWLE	STTVSV	
bovine coronavirus pol 1ab (3441)		VQDYIQSV	FANLYAAILNN	-----CNWFEVQSDKCSV	
Human corona 229E pol 1ab (3159)		SANQMLTV	VVAFLAAILNG	-----CTWLLKGEKLFV	
Murine hepatitis pol 1ab (3528)		VQDYTOTV	VAWFAHLSFNR	-----CNWFEVQSDSCSE	
Consensus (3589)		VQDYIQTVN	VVAWLYAAILN		CNWFLQSDKCSV
Section 94					
	(3628)	3628	3640	3650	3666
avian infectious bronchitis pol 1ab (3011)		DDYIKNAGNGET	TPSTGTATTKISAT	EDVDCKLIRTI	
bovine coronavirus pol 1ab (3474)		EDFNVAISNGT	SOVKSDIVDALASMLC	SLETLGAAT	
Human corona 229E pol 1ab (3192)		EHYNERAQCNG	TAMNGEDAFSILAAKI	TCVERILHAAT	
Murine hepatitis pol 1ab (3561)		EEFNVAISNGT	SSIKADLVIDAASM	TVEQVTAAT	
Consensus (3628)		EDFNVAISNGF	SAIKADLVIDALAAMTGVSVEKLLAAI		
Section 95					
	(3667)	3667	3680	3690	3705
avian infectious bronchitis pol 1ab (3050)		MMKNSQWGGDP	PHQYNFEDEBTBSVEN	IGVRSQK	-
bovine coronavirus pol 1ab (3513)		KRLKNGFGQ	ROIMGSCSTEDLTPSDVYQ	LACIKQSK	
Human corona 229E pol 1ab (3231)		QMLNNGFGGK	QILSYSSLDHDFSINE	VPKMFVNLQK	-
Murine hepatitis pol 1ab (3600)		KRLKSGFGQ	KQILSCVLEDELTTPSDVYQ	LACVKKQSK	
Consensus (3667)		KVLNSGFGGKQIL	SGSCSLEDELTPSDVYQQLAGVKLQSK		
Section 96					
	(3706)	3706	3720	3730	3744
avian infectious bronchitis pol 1ab (3088)		-SFVRKATIS	-FWSRCVFACE	EFVLCAIVLFTAVPLKEY	
bovine coronavirus pol 1ab (3552)		RTRIVKGI	VCWIMASTEFL	ESCITAEVKWTMFMVYTTNM	
Human corona 229E pol 1ab (3269)		-GKTSMFKS	ISLFAGEFVMEWAE	LFVYTUTLVWNGEL	
Murine hepatitis pol 1ab (3639)		RTRVIKGT	CCWILASTEFL	ECSTISAEVKWTMFMVYTTNM	
Consensus (3706)		RTRVIKGT	CWILASTEFL	CFIISLEVKWTMFMVYTTFM	

30/199

FIGURE 4A (contd.)

Section 97					
	(3745)	3745	3750	3760	3770 3783
avian infectious bronchitis pol 1ab (3125)		VYAAMILLMAVLEISFTV	AVMAVMDTEHPTLTITVIG		
bovine coronavirus pol 1ab (3591)		LSITFCALCVISLAMDIV	FKHLYLTMYTLEVLFTLLEYN		
Human corona 229E pol 1ab (3307)		TPFMILLVALSLCLTFVVR	KKVLEPQVFLDPSIIVAATQ		
Murine hepatitis pol 1ab (3678)		EGVTLGALCTVSEAMLLTK	KKHLYLTMYTLPVLCITLTY		
Consensus (3745)		LITICLLCLVSEAMLLVKKHLYLTMFILPVLITLIYN			
Section 98					
	(3784)	3784	3790	3800	3810 3822
avian infectious bronchitis pol 1ab (3164)		VCAEVPFIYNTLISQVV	IFLSQWYDPVVEDTMVPWMFLP		
bovine coronavirus pol 1ab (3630)		NYLVVYKQTERGYVYAWLS	SYVMPSEVETTYTDEVTYGMLD		
Human corona 229E pol 1ab (3346)		NCAWDYHVTKVLAEKFDYN	VSVMOMDIQGFVNIFICDFM		
Murine hepatitis pol 1ab (3717)		NYLVVYKQSERGLAYAW	SHFVPAVDYTYMDEVTYGVVLE		
Consensus (3784)		NYLVVYKQTERLIAYAWLSVSVPAVDYTYDEVIYGLLL			
Section 99					
	(3823)	3823	3830	3840	3850 3861
avian infectious bronchitis pol 1ab (3203)		LVTDTAFKCVQGCYMNSFNTS	LLMMLYQFVKLGFEVLYTSS		
bovine coronavirus pol 1ab (3669)		LTGMVFVTLRSINHD	-----	LFSEIMVGRVISVV	
Human corona 229E pol 1ab (3385)		ALLHTMRFAKER	-----	CTHWCTYBFSLL	
Murine hepatitis pol 1ab (3756)		LVA MVFVTLRSINHD	-----	VFSTMFVGRLLVSLV	
Consensus (3823)		LVL MVFVTLRSINHD		LFSEI LVGRLLVSLV	
Section 100					
	(3862)	3862	3870	3880	3890 3900
avian infectious bronchitis pol 1ab (3242)		NLTAYIEGHWELFE	LVHTTVLANVSSNSLIGLFVFKC		
bovine coronavirus pol 1ab (3699)		SLWYMGSNLEEEILLMLAS	LFCTYTWTATLSMAAAKVLA		
Human corona 229E pol 1ab (3409)		AVLYTALYSYDYMSLLVMLL	CAISNEWYTGALIFRICRF		
Murine hepatitis pol 1ab (3786)		SMWYFGANLEEEVLLFLT	SLFCTYTWTITLSIATAKVIA		
Consensus (3862)		SLWY GSNLEEEVLLLLMSLFCTYTWTITLSIA AKVIA			
Section 101					
	(3901)	3901	3910	3920	3939
avian infectious bronchitis pol 1ab (3281)		AKWMLYYCNATYLN	NYVIMAVMVNGICWLCCTCFGLYWN		
bovine coronavirus pol 1ab (3738)		KWVAVNVLYETDIPQIK	LVLCYLFICYTISCIWGLFSL		
Human corona 229E pol 1ab (3448)		GVAFLPVEVVS	YFDGVKTVDLFYMLL	EFVSCMYGLLYW	
Murine hepatitis pol 1ab (3825)		KWLAVNVLYETDIPQIK	LVLLSYDCIGYVCCG	INCLISL	
Consensus (3901)		KWLALNVLYFTYIPQIKLVLL YLCIGYVCCCYWGLLSW			
Section 102					
	(3940)	3940	3950	3960	3978
avian infectious bronchitis pol 1ab (3320)		VHKVEGLTLCKYNEKMS	VDQYRIMCLHKE	NRPKTVWEVF	
bovine coronavirus pol 1ab (3777)		MNSIERMPLGVYNYKT	VQELRYMNANGLRPPKNSFEAL		
Human corona 229E pol 1ab (3487)		INRFCKCTGVVDECV	PAEFKLVANGLNA	NGPEDAL	
Murine hepatitis pol 1ab (3864)		INSTERMPLGVYNYKT	VQELRYMNANGLRPP	RNSFEAL	
Consensus (3940)		INSIERMTLGVYNFKISVQELRYMNANGLRPPKNSFEAL			

31/199

FIGURE 4A (contd.)

Section 103						
	(3979)	3979	3990	4000	4017	
avian infectious bronchitis pol 1ab (3359)		STNIIITQELGGDRVLPPTATVPAKESDVKCTTVVLMOLLT				
bovine coronavirus pol 1ab (3816)		MLNFKLLIGGGVPTTEVVSQFOSKLTQVKCANVVLINCGO				
Human corona 229E pol 1ab (3526)		FLSEKLMELGGPTIRVSTVSKLTDLCTNNVLMCILS				
Murine hepatitis pol 1ab (3903)		MLNEKLLGGTGGVPTIEVSQFOSKLTQVKCANVVLINCGO				
Consensus (3979)		MLNFKLLGIGGVRVIEVSTVQS KLTQVKCTNVVLLNCLQ				
Section 104						
	(4018)	4018	4030	4040	4056	
avian infectious bronchitis pol 1ab (3398)		KLNVETAEKMHVTLVELHKKTLASDLVGECDNLEGLIT				
bovine coronavirus pol 1ab (3855)		HLHVASTSKLWQYCSILLNEELATSDLGVAPEKTAQDLT				
Human corona 229E pol 1ab (3565)		NMNTASTSKLWALCVEMHKKNLCDLPEFAQELLTADEA				
Murine hepatitis pol 1ab (3942)		HLHVTASNSKLWQYCSILLNEELATSDLSVAFDKLAQLLV				
Consensus (4018)		HLNIASNSKLWQYCVTLHNKILATSDLGVAFDKLLQLLI				
Section 105						
	(4057)	4057	4070	4080	4095	
avian infectious bronchitis pol 1ab (3437)		TLECIDSTED-----TSEYCDITIKRSTVLSVTQETS				
bovine coronavirus pol 1ab (3894)		VLFANPAAVDSKCLTSIEEVCDDYAKDNTVLQALQSEFV				
Human corona 229E pol 1ab (3604)		FFLSKHSIDFG-----LGDELVSFFENDSTPLSVASSIV				
Murine hepatitis pol 1ab (3981)		VLFANPAAVDSKCLASTEIEVSDDYVRDNTVLQALQSEFV				
Consensus (4057)		VLFANPAAVDSKCL SIEEVCDDYLKDNTVLQALQSEFV				
Section 106						
	(4096)	4096	4110	4120	4134	
avian infectious bronchitis pol 1ab (3470)		HTPVAEYTRAKNLGKVLVDSKNGGVTOQFLAAYKKA				
bovine coronavirus pol 1ab (3933)		NMASFVPTFAKKNLDEAPSSGGSAN---QQQIKOLEKAC				
Human corona 229E pol 1ab (3637)		GMPSEVAETTRQFYENAVANGSS---PQITKOLEKAM				
Murine hepatitis pol 1ab (4020)		NMASFVEFLAKKNLDEAKASSGSAN---QQQIKOLEKAC				
Consensus (4096)		NMPSEVEYELAKKNYDEARASSGSAN QQQIKOLEKAC				
Section 107						
	(4135)	4135	4140	4150	4160	4173
avian infectious bronchitis pol 1ab (3509)		NIAKSVEDPDLAYQKKLDSMAERAMTMMETFAVTDERRA				
bovine coronavirus pol 1ab (3969)		ELAKSAYERDRAVARKLERMADLALTNNMYKEARINDKKS				
Human corona 229E pol 1ab (3672)		NVALAEEDFESSVOKKLNRIEQAAAAAMYLARAVNRKS				
Murine hepatitis pol 1ab (4056)		ELAKSAYERDRAVARKLERMADLALTNNMYKLARINDKKS				
Consensus (4135)		NIAKSAFDRDRAVQKKLERMADLALTNNMYKEARINDKKS				
Section 108						
	(4174)	4174	4180	4190	4200	4212
avian infectious bronchitis pol 1ab (3548)		KVVSALQTLLESMRLKLDNQALNSILDNAVKGCVPLNAI				
bovine coronavirus pol 1ab (4008)		KVVSALQTLLESMVRKLDNQALNSILDNAVKGCVPLNAI				
Human corona 229E pol 1ab (3711)		KVVSAMNSLTLEGLRRDLMSSVDTILNMAKNVPLNSVI				
Murine hepatitis pol 1ab (4095)		KVVSALQTLLESMVRKLDNQALNSILDNAVKGCVPLNAI				
Consensus (4174)		KVVSALQTLLESMRLKLDNQALNSILDNAVKGCVPLNAI				

FIGURE 4A (contd.)

Section 109					
	(4213)	4213	4220	4230	4240 4251
avian infectious bronchitis pol 1ab (3587)		PIMCSNRETLVLPDPETWVKCEGWHVYISTVYVNIIDTV			
bovine coronavirus pol 1ab (4047)		PSLAANTLTITVEDKSVYDQVVDNVYVTIAGNANQIQTI			
Human corona 229E pol 1ab (3750)		PATSAAPRIVVVDHDSFVKMMVDGEVHYAGVWVTEQEV			
Murine hepatitis pol 1ab (4134)		PSLTISNTLTITVEDKQVEDQVVDNVYVTIAGNVWHIQFI			
Consensus (4213)		PSLSANTLTIIIVPDKDVFVQVVDNVYVTYAGVVWNIQTI			
Section 110					
	(4252)	4252	4260	4270	4280 4290
avian infectious bronchitis pol 1ab (3626)		TLADCTELHPTSTGSLTYCISGANIAWPKMNETRNGH			
bovine coronavirus pol 1ab (4086)		QISDCTNKQNEISD-----DCNWPVETIAHRHNE			
Human corona 229E pol 1ab (3789)		KDNDGKNVHLKDMTK-----ENQEI-VWPTILTCE			
Murine hepatitis pol 1ab (4173)		QADGCAVKQNEITDV-----NSTWPTVTAANRHNE			
Consensus (4252)		QDADGNTKQNEIS			N NWPLVI LNRHNE
Section 111					
	(4291)	4291	4300	4310	4329
avian infectious bronchitis pol 1ab (3665)		NKMDVVLO--NLLEPHGMKTKACVAGVDAQHCSVEISKCY			
bovine coronavirus pol 1ab (4116)		VSATVLO--NLLEPAKLKTQVNS-CPDQTCNTPTQCY			
Human corona 229E pol 1ab (3819)		RVYKIQ--NLLEPGMKVKRATKG-EGDGGITSEGNALY			
Murine hepatitis pol 1ab (4203)		VSTVVLO--NLLEPEQKLRTOVNS-GSDMNCNTPTQCY			
Consensus (4291)		VSV VLQ NNELMPAKLKTQVNS G DA CNTPTQCY			
Section 112					
	(4330)	4330	4340	4350	4368
avian infectious bronchitis pol 1ab (3704)		TNISGHSVVAATSSNPNNDKVASFLNEA-NQHYVDLDF			
bovine coronavirus pol 1ab (4153)		NNSNNGKIVY-ILSDVDGLKYTKILKDDGNFVVLELDF			
Human corona 229E pol 1ab (3855)		NNEGGRAFMY-YVETKEGMYVKWERDS-VVTVLELDF			
Murine hepatitis pol 1ab (4240)		NTTGTGKIVY-ILSDCDGLKYTKIVKED-NCVLELDF			
Consensus (4330)		NNSGGGKIVYAILSD PGLKYTKILKDDGN VVLELDPP			
Section 113					
	(4369)	4369	4380	4390	4407
avian infectious bronchitis pol 1ab (3743)		CKEFGMKVGKVEVYLY-IRNTRSTVRGMVLEATSNVTV			
bovine coronavirus pol 1ab (4192)		CKRTVODVKGGLKIKLYLVKGNLTARWVQILTSSTVR			
Human corona 229E pol 1ab (3893)		CRVVDLPTPTGPQIKLYLVNLLNNLRGAVLYGIGATVR			
Murine hepatitis pol 1ab (4279)		CKRSVDVKGGLKIKLYLVKGNLTARWVQILTSSTVR			
Consensus (4369)		CKFSVDVKGGLKIKLYLVKNCNTLARGVVLGTISSTVR			
Section 114					
	(4408)	4408	4420	4430	4446
avian infectious bronchitis pol 1ab (3782)		LUSKGHELEEVDAVGTLSTCSFAVDADATYCKYVAACNQ			
bovine coronavirus pol 1ab (4231)		LQAG-TATEYASNSAILSLCAESVDKKTYLDEIQQGGT			
Human corona 229E pol 1ab (3932)		LQAG-KQTEVSNSHLLTHCSAFLPAAVLDVAKQAK			
Murine hepatitis pol 1ab (4318)		LQAG-TATEYASNSAILSLCAESVDKKTYLDEIQQGGV			
Consensus (4408)		LQAG TATEYVSNAILSLCAFAVDPKKTYLDYIKQGG			

FIGURE 4A (contd.)

Section 115				
	(4447)	4447	4460	4470 4485
avian infectious bronchitis pol 1ab (3821)		PDGNTVHNCSEPAITTSKPEPTDPS	YGGASVCH	
bovine coronavirus pol 1ab (4269)		PTANQYKMLCDHACTGMAITVKPDATTNQDSYGGASVCH		
Human corona 229E pol 1ab (3970)		PVGNOVRMLTNGSSSQPAITCTIDSNITTDITYGGASVCH		
Murine hepatitis pol 1ab (4356)		PVTNCTMLCDHACTGMAITLKPEATTNQDSYGGASVCH		
Consensus (4447)		PVGNCVVKMLTDHAGSGMAITIKPDATTNQDSYGGASVCH		
Section 116				
	(4486)	4486	4500	4510 4524
avian infectious bronchitis pol 1ab (3860)		YCRARVEHP	DVDGLCKLRKRFVQVVGKIKDPVSYV	
bovine coronavirus pol 1ab (4308)		YCRARVEHP	DVDGLCKLRKRFVQVVGKIKDPVSYV	
Human corona 229E pol 1ab (4009)		YCRARVEHP	DVDGLCKLRKRFVQVVGKIKDPVSYV	
Murine hepatitis pol 1ab (4395)		YCRARVEHP	DVDGLCKLRKRFVQVVGKIKDPVSYV	
Consensus (4486)		YCRARVEHP	DVDGLCKLRKRFVQVVGKIKDPVSYV	
Section 117				
	(4525)	4525	4530	4540 4550 4563
avian infectious bronchitis pol 1ab (3899)		LRNKCT	QCGIGYGCQDGLRQPKSSVQSVAGASDFD	
bovine coronavirus pol 1ab (4343)		LRNKCT	QCGIGYGCQDGLRQPKSSVQSVAGASDFD	
Human corona 229E pol 1ab (4044)		LRNKCT	QCGIGYGCQDGLRQPKSSVQSVAGASDFD	
Murine hepatitis pol 1ab (4430)		LRNKCT	QCGIGYGCQDGLRQPKSSVQSVAGASDFD	
Consensus (4525)		LRNKCT	QCGIGYGCQDGLRQPKSSVQSVAGASDFD	
Section 118				
	(4564)	4564	4570	4580 4590 4602
avian infectious bronchitis pol 1ab (3938)		TNELLNRVRS	SS-EARLEPLASCDPPDVVK	ATDVC KES
bovine coronavirus pol 1ab (4373)		TNELLNRVRS	SS-EARLEPLASCDPPDVVK	ATDVC KES
Human corona 229E pol 1ab (4072)		TNELLNRVRS	SS-EARLEPLASCDPPDVVK	ATDVC KES
Murine hepatitis pol 1ab (4460)		TNELLNRVRS	SS-EARLEPLASCDPPDVVK	ATDVC KES
Consensus (4564)		TNELLNRVRS	SS-EARLEPLASCDPPDVVK	ATDVC KES
Section 119				
	(4603)	4603	4610	4620 4630 4641
avian infectious bronchitis pol 1ab (3976)		AGMFQNLKRNAT	FORVDEDEDGNLEYL	SYFVVKQTP
bovine coronavirus pol 1ab (4412)		AGMFQNLKRNAT	FORVDEDEDGNLEYL	SYFVVKQTP
Human corona 229E pol 1ab (4109)		AGMFQNLKRNAT	FORVDEDEDGNLEYL	SYFVVKQTP
Murine hepatitis pol 1ab (4499)		AGMFQNLKRNAT	FORVDEDEDGNLEYL	SYFVVKQTP
Consensus (4603)		AGMFQNLKRNAT	FORVDEDEDGNLEYL	SYFVVKQTP
Section 120				
	(4642)	4642	4650	4660 4670 4680
avian infectious bronchitis pol 1ab (4015)		SNYEHKSC	EDIKSS-EVTDIDT	EVENKN---TYNTS
bovine coronavirus pol 1ab (4447)		SNYEHKSC	EDIKSS-EVTDIDT	EVENKN---TYNTS
Human corona 229E pol 1ab (4140)		SNYEHKSC	EDIKSS-EVTDIDT	EVENKN---TYNTS
Murine hepatitis pol 1ab (4534)		SNYEHKSC	EDIKSS-EVTDIDT	EVENKN---TYNTS
Consensus (4642)		SNYEHKSC	EDIKSS-EVTDIDT	EVENKN---TYNTS

FIGURE 4A (contd.)

Section 121				
	(4681)	4681	4690	4700
avian infectious bronchitis pol 1ab (4050)		QRNIRKYYTMMDFCYALRHFPKJCEVLKETLVTYGCIEDY		4719
bovine coronavirus pol 1ab (4486)		KDLTRYTALFLCYALRHFDNRDCMELCDILSIYAGCEQS		
Human corona 229E pol 1ab (4179)		QDLTRYTMMDLCEALRNDEKDCMFKELVLTGCCSTB		
Murine hepatitis pol 1ab (4573)		KDLTRYTALFLCYALRHFDNRDCSTLKEITLVYAECEES		
Consensus (4681)		QDLTRYTMDLFCYALRHFDNRDCMELKEILVYACCEDS		
Section 122				
	(4720)	4720	4730	4740
avian infectious bronchitis pol 1ab (4089)		HPKWFEEENEDYDPTENSRYYYVMLARMGETVPRRLNAI		4758
bovine coronavirus pol 1ab (4525)		Y----ETKTDWYDFVSNPDIINVKKLGPINRRLNVAI		
Human corona 229E pol 1ab (4218)		Y----FEMKNNFLPTLEEDTHRVYAALSKVMANAMDKCM		
Murine hepatitis pol 1ab (4612)		Y----EOKKDWDFVSNPDIINVKKLGPINRRLNVAI		
Consensus (4720)		YFEKKDWYDPIENPDIINVKKLGPINRRLNVAI		
Section 123				
	(4759)	4759	4770	4780
avian infectious bronchitis pol 1ab (4128)		EEGNLMMEKGYAVLTLDNQDLNGKFYDEGDFVKTAAGC		4797
bovine coronavirus pol 1ab (4560)		EEADKIIEVLLYQPLLDLNDINRWYDFDYVIAAPGC		
Human corona 229E pol 1ab (4253)		AHCDEMELKGVVLLLDLNLNNEIFGDFVLCPPHM		
Murine hepatitis pol 1ab (4647)		KUADAIIEAGLYVLLLDNQLYGGWYDFGDFVKTVRGC		
Consensus (4759)		EFADLVEKGLVGVLTLDNQDLNGKFYDEGDFVKTAAGC		
Section 124				
	(4798)	4798	4810	4820
avian infectious bronchitis pol 1ab (4167)		GVPVFDTSYYSYMMPLTMTHALDSELFVN D		4836
bovine coronavirus pol 1ab (4599)		GVATADSYYSYMMPLTMTHALDSELFVN-----NAYRL		
Human corona 229E pol 1ab (4292)		GTPYCTSYYSYMMPLTMTHALDSELFVN-----CTYRE		
Murine hepatitis pol 1ab (4686)		GVAVADSYYSYMMPLTMTHALDSELFVN-----CTYRE		
Consensus (4798)		GVPVADSYYSYMMPLTMTHALDSELFVN D		NAYKS
Section 125				
	(4837)	4837	4850	4860
avian infectious bronchitis pol 1ab (4205)		FDLLQYDFTDHKLELENKYEKHWSQDYHPNTVDC		4875
bovine coronavirus pol 1ab (4633)		FLLVQYDFDTHKLELENKYEKHWSQDYHPNTVDC		
Human corona 229E pol 1ab (4331)		FLLVQYDFDTHKLELENKYEKHWSQDYHPNTVDC		
Murine hepatitis pol 1ab (4720)		FLLVQYDFDTHKLELENKYEKHWSQDYHPNTVDC		
Consensus (4837)		FDLLQYDFTDHKLELENKYEKHWSQDYHPNTVDC		DDRC
Section 126				
	(4876)	4876	4890	4900
avian infectious bronchitis pol 1ab (4244)		IITHCANFNILFSTVIPTNCEGPLVRQIFVDGVPFVVSIG		4914
bovine coronavirus pol 1ab (4672)		IITHCANFNILFSTVIPTNCEGPLVRQIFVDGVPFVVSIG		
Human corona 229E pol 1ab (4370)		IITHCANFNILFSTVIPTNCEGPLVRQIFVDGVPFVVSIG		
Murine hepatitis pol 1ab (4759)		IITHCANFNILFSTVIPTNCEGPLVRQIFVDGVPFVVSIG		
Consensus (4876)		IITHCANFNILFSTVIPTNCEGPLVRQIFVDGVPFVVSIG		

FIGURE 4A (contd.)

	Section 127				
	(4915)	4915	4920	4930	4940 4953
avian infectious bronchitis pol 1ab (4283)		YHS	ELGVIMNQDNTMSFSKMGLSOLMOFVGERALLVGT		
bovine coronavirus pol 1ab (4711)		YHY	ELGVMMMDVDTHRYRLSLKDLLLYAADI ALHVAS		
Human corona 229E pol 1ab (4409)		YHE	KQILVWKKVNTHTSTRLTITELLOFVTDPTETIVAS		
Murine hepatitis pol 1ab (4798)		YHY	ELGVMMMDVDTHRYRLSLKDLLLYAADI ALHVAS		
Consensus (4915)		YHY	KELGVMMMDVDTHRYRLSLKDLLQFVADPALHVAS		
	Section 128				
	(4954)	4954	4960	4970	4980 4992
avian infectious bronchitis pol 1ab (4322)		SNN	LVDRRLSLESVCATPSLITHQTVRPGHENADLYDFA		
bovine coronavirus pol 1ab (4750)		ASAL	YDERECCEFAATRSQVKFQTVRPGNANODEYDFI		
Human corona 229E pol 1ab (4448)		SPA	LVFKLVGSAVASTGLTSQTVRPGHNNEFYDML		
Murine hepatitis pol 1ab (4837)		ASAL	YDERECCEFAATRSQVKFQTVRPGNANODEYDFI		
Consensus (4954)		ASAL	VDLRTCCFSVAAITSGVTFQTVKPGNFNQDFYDFI		
	Section 129				
	(4993)	4993	5000	5010	5020 5031
avian infectious bronchitis pol 1ab (4361)		EKA	MPKLESLIPKATMPQTNNAINVDLRNRRT		
bovine coronavirus pol 1ab (4789)		LSK	GLLEKLSVDEKHEFTQDGNAAITDYNYYKYNLPT		
Human corona 229E pol 1ab (4487)		RSQ	FEDELSEDTKKHETAKGDAIKEDARVRRPT		
Murine hepatitis pol 1ab (4876)		LSK	GLLEKLSVDEKHEFTQDGNAAITDYNYYKYNLPT		
Consensus (4993)		LSK	GLLEKLSVDEKHEFTQDGNAAITDYNYYKYNRPT		
	Section 130				
	(5032)	5032	5040	5050	5060 5070
avian infectious bronchitis pol 1ab (4400)		MEI	IKQLLECELYTSKYTECEYEGGCI PASQVVMNLDKLS		
bovine coronavirus pol 1ab (4828)		MVD	IKQLLEVLEVYKYTEITDCECTPASQVIVNNYDLS		
Human corona 229E pol 1ab (4526)		MEI	IGGARVAYQAAKEDCEGGLTSREVMETNLNLS		
Murine hepatitis pol 1ab (4915)		MVD	IKQLLEVLEVYKYTEITDCECTPASQVIVNNYDLS		
Consensus (5032)		MVD	IKQLLEVLEVYKYTEITDCECTPASQVIVNNYDLS		
	Section 131				
	(5071)	5071	5080	5090	5109
avian infectious bronchitis pol 1ab (4439)		AGY	PENKFGKARLYEALSFEEQDEIFAYTKRNVLP TLT		
bovine coronavirus pol 1ab (4867)		AGY	PENKFGKARLYEALSFEEQDEIFAYTKRNVLP TLT		
Human corona 229E pol 1ab (4565)		AGW	LNKFGKAGLYEALSFEEQDEIFAYTKRNVLP TLT		
Murine hepatitis pol 1ab (4954)		AGY	PENKFGKARLYEALSFEEQDEIFAYTKRNVLP TLT		
Consensus (5071)		AGY	PENKFGKARLYEALSFEEQDEIFAYTKRNVLP TLT		
	Section 132				
	(5110)	5110	5120	5130	5148
avian infectious bronchitis pol 1ab (4477)		QMN	LKYAISAKNRARTVAGVSI LSTMTGRQFHQKCLKSI		
bovine coronavirus pol 1ab (4906)		QMN	LKYAISAKNRARTVAGVSI LSTMTGRQFHQKCLKSI		
Human corona 229E pol 1ab (4604)		QMN	LKYAISAKNRARTVAGVSI LSTMTGRQFHQKCLKSI		
Murine hepatitis pol 1ab (4993)		QMN	LKYAISAKNRARTVAGVSI LSTMTGRQFHQKCLKSI		
Consensus (5110)		QMN	LKYAISAKNRARTVAGVSI LSTMTGRQFHQKCLKSI		

FIGURE 4A (contd.)

Section 133						
	(5149)	5149	5160	5170	5187	
avian infectious bronchitis pol 1ab (4516)		VNT	RNASVNLGTELEFYGGWDNMLRRLIQGSEDPLEMLMD			
bovine coronavirus pol 1ab (4945)		AAT	RCMPVATGCTTKFYGGNDMLRRLIKDYDNPVLGND			
Human corona 229E pol 1ab (4643)		VAT	INATVVLGTTKFGGWNNMLKNI MADVDDPKMGWD			
Murine hepatitis pol 1ab (5032)		AAT	RCMPVATGTEKFGGWNNMLRRLIKDVSFVIMGND			
Consensus (5149)		VAT	RNVFPVVGTTKFGGWNNMLRRLIKDVDDPVLMGWD			
Section 134						
	(5188)	5188	5200	5210	5226	
avian infectious bronchitis pol 1ab (4555)		YPK	CDRAMPNILRIVSSLVLARKHEACSSQSDRFYRLAN			
bovine coronavirus pol 1ab (4984)		YPK	CDRAMPNILRIVSSLVLARKHEACSSQSDRFYRLAN			
Human corona 229E pol 1ab (4682)		YPK	CDRAMPNILRIVSSLVLARKHDSGCCSHEDREYRLAN			
Murine hepatitis pol 1ab (5071)		YPK	CDRAMPNILRIVSSLVLARKHDSGCCSHEDREYRLAN			
Consensus (5188)		YPK	CDRAMPNILRIVSSLVLARKHDSGCCS SDRFYRLAN			
Section 135						
	(5227)	5227	5240	5250	5265	
avian infectious bronchitis pol 1ab (4594)		ECA	QVLSEITMCGGCGYVVKPGGTSSGDATTAFAFANSVFN			
bovine coronavirus pol 1ab (5023)		ECA	QVLSEITMCGGCGYVVKPGGTSSGDATTAFAFANSVFN			
Human corona 229E pol 1ab (4721)		ELA	QVITLVYVSNIGETFRGGTSSGDATTAFAFANSVFN			
Murine hepatitis pol 1ab (5110)		ECA	QVLSEITMCGGCGYVVKPGGTSSGDATTAFAFANSVFN			
Consensus (5227)		ECA	QVLSEITMCGGCGYVVKPGGTSSGDATTAFAFANSVFN			
Section 136						
	(5266)	5266	5280	5290	5304	
avian infectious bronchitis pol 1ab (4633)		IQAT	SANVARLLSVITRDIVYDNIKSLQYSTYQOYVPRV			
bovine coronavirus pol 1ab (5062)		CQAV	SANVCALMSCNGNKIEDLSIRALQKRRLSNVYRAD			
Human corona 229E pol 1ab (4760)		EQAV	SANVCALMSCNGNKIEDLSIRALQKRRLSNVYRAD			
Murine hepatitis pol 1ab (5149)		CQAV	SANVCALMSCNGNKIEDLSIRALQKRRLSNVYRAD			
Consensus (5266)		CQAV	SANVCALLSVNG KIEDLSIKALQKRRLSNVYRAD			
Section 137						
	(5305)	5305	5310	5320	5330	5343
avian infectious bronchitis pol 1ab (4672)		NVD	PAFVSEFYEFNLKHF	SMMILSDDGVVCYNSTYASKG		
bovine coronavirus pol 1ab (5101)		MVLS	TAFTETLLEFLNAHTSMMILSDDGVVCYNSTYASKG			
Human corona 229E pol 1ab (4799)		NVLS	ETDDEFGYLOKHFSMMILSDDGVVCYNSTYASKG			
Murine hepatitis pol 1ab (5188)		NVD	PAFVSEFYEFNLKHF	SMMILSDDGVVCYNSTYASKG		
Consensus (5305)		NVD	PAFVSEFYEFNLKHF	SMMILSDDGVVCYNSTYASKG		
Section 138						
	(5344)	5344	5350	5360	5370	5382
avian infectious bronchitis pol 1ab (4711)		LVAD	TAFAKATDYVNGVEMSTAKGTIEDLSIGVLRGND			
bovine coronavirus pol 1ab (5140)		YIAN	SAFQOQVLYYQNNVFMSEAKCWVE	DIEKGPHEFC		
Human corona 229E pol 1ab (4838)		YIAD	TAFAKATDYVNGVEMSTAKGTIEDLSIGVLRGND			
Murine hepatitis pol 1ab (5227)		YIAN	SAFQOQVLYYQNNVFMSEAKCWVE	DIEKGPHEFC		
Consensus (5344)		YIAN	SAFQOQVLYYQNNVFMSEAKCWVE	DIEKGPHEFC		

FIGURE 4A (contd.)

Section 139					
	(5383)	5383	5390	5400	5410 5421
avian infectious bronchitis pol 1ab (4750)		SCHTMLV	VDGEPKYL	YPDTSR	LGACMPYDDVD
bovine coronavirus pol 1ab (5179)		SCHTMLVKMDGDDVYL	YPDPSRI	LGAGCFVDDLL	TD
Human corona 229E pol 1ab (4877)		SCHTMQIVDENGKYYL	YPDASH	LSAGVFD	DDTTADA
Murine hepatitis pol 1ab (5266)		SCHTMLVKMDGDEVYL	YPDPSR	LGAGCFVDDLL	TD
Consensus (5383)		SQHTMLVKMDGDDVYL	YPDPSRI	LGAGVFVDDLL	KTDS
Section 140					
	(5422)	5422	5430	5440	5450 5460
avian infectious bronchitis pol 1ab (4789)		VAVMPEAYTALA	AYPLVH	ENEENEYK	KVEFVLLAYTRK
bovine coronavirus pol 1ab (5218)		VLLIERFVSLAIDAY	PLVYHENE	EYQK	YFRVMLEYTRK
Human corona 229E pol 1ab (4916)		VLLIERFVSLAIDAY	PLSKHPK	PEERK	AYALLDWVKH
Murine hepatitis pol 1ab (5305)		VLLIERFVSLAIDAY	PLVYHENE	EYQK	YFRVMLEYTRK
Consensus (5422)		VLLIERFVSLAIDAY	PLVYHENPEY	QKVERVYLEY	IKKL
Section 141					
	(5461)	5461	5470	5480	5499
avian infectious bronchitis pol 1ab (4828)		YQENSONMTMDYS	FVMDIDKGS	KWECE	TMENMYRAPIT
bovine coronavirus pol 1ab (5257)		YNDLGNQILDSY	VILSTCDG	GKFTDES	YKNMYLRSAV
Human corona 229E pol 1ab (4955)		NKTINEGVLESE	VTILDEHES	KWDES	YASHLEKSTV
Murine hepatitis pol 1ab (5344)		YNDLGNQILDSY	VILSTCDG	GKFTDES	YKNMYLRSAV
Consensus (5461)		YNDLGNQILDSY	VILSTCDGSK	FWDES	FYKNMYLRSTV
Section 142					
	(5500)	5500	5510	5520	5538
avian infectious bronchitis pol 1ab (4867)		LGSCGVGVCS	THIRGGNC	IRKPFLL	CCGTHHNMHT
bovine coronavirus pol 1ab (5296)		MQSVGACVVCSS	QTSIRGCS	IRKPFLL	CCGTHHNMHT
Human corona 229E pol 1ab (4994)		LQAAGLQVVCSS	QTSIRGCS	IRKPFLL	CCGTHHNMHT
Murine hepatitis pol 1ab (5383)		LQSVGACVVCSS	QTSIRGCS	IRKPFLL	CCGTHHNMHT
Consensus (5500)		LQSVGACVVCSS	QTSIRGCS	IRKPFLL	CCGTHHNMHT
Section 143					
	(5539)	5539	5550	5560	5577
avian infectious bronchitis pol 1ab (4906)		DLKYNVLSIS	SPYVCNS	PGCDVND	VTKLYLGGMSYYCEDHK
bovine coronavirus pol 1ab (5335)		DLKYNVLSIS	SPYVCNS	PGCDVND	VTKLYLGGMSYYCEDHK
Human corona 229E pol 1ab (5033)		DLKYNVLSIS	SPYVCNS	PGCDVND	VTKLYLGGMSYYCEDHK
Murine hepatitis pol 1ab (5422)		DLKYNVLSIS	SPYVCNS	PGCDVND	VTKLYLGGMSYYCEDHK
Consensus (5539)		DLKYNVLSIS	SPYVCNS	PGCDVND	VTKLYLGGMSYYCEDHK
Section 144					
	(5578)	5578	5590	5600	5616
avian infectious bronchitis pol 1ab (4945)		PNLEIPVVSNGTY	GLYRANGA	GSSENVD	DFNOLATTNVS
bovine coronavirus pol 1ab (5374)		PQYSFPLVSNM	GVFGLYKQ	SCTGSPY	IDDFNKIASCKWT
Human corona 229E pol 1ab (5072)		PNLEIPVVSNGTY	GLYRANGA	GSSENVD	DFNOLATTNVS
Murine hepatitis pol 1ab (5461)		PQYSFPLVSNM	GVFGLYKQ	SCTGSPY	IDDFNKIASCKWT
Consensus (5578)		PQYSFPLVSNM	GVFGLYKQ	SCTGSPY	IDDFNKIASCKWT

FIGURE 4A (contd.)

Section 145						
	(5617)	5617	5630	5640	5655	
avian infectious bronchitis pol 1ab (4984)		IVEPYLEANRCSDSERRFAAEYVKATDELHQDEASAEV				
bovine coronavirus pol 1ab (5413)		DVDDYILANECTERERKLFPAEETQKATEAEKQSYASATI				
Human corona 229E pol 1ab (5111)		DIIDYKLANDAKESERLFAAEYVKAKESVSSSYATATE				
Murine hepatitis pol 1ab (5500)		EVDDYILANECTERERKLFPAEETQKATEAEKQCYASATI				
Consensus (5617)		DVDDYILANECTESLKLFAAEYVKATEEAFKQSYASATI				
Section 146						
	(5656)	5656	5670	5680	5694	
avian infectious bronchitis pol 1ab (5023)		REIVSDRELILSWEIPGTRPEINRUYVETGYHFTKNSKV				
bovine coronavirus pol 1ab (5452)		QELVSERELILISWEIGVKPPLNKNYVETGYHFTKNSKT				
Human corona 229E pol 1ab (5150)		KEIVGPKLLILLNSESNAKFPPLNRSTCTCEQIKDSKF				
Murine hepatitis pol 1ab (5539)		REIVSDRELILSWEIGVKPPLNKNYVETGYHFTKNSKT				
Consensus (5656)		REIVSDRELILSWEIGVKPPLNKNYVETGYHFTKNSKT				
Section 147						
	(5695)	5695	5700	5710	5720	5733
avian infectious bronchitis pol 1ab (5062)		QLQDETLEEGEGADV-VYKATSAKTSVDTFVITSHN				
bovine coronavirus pol 1ab (5491)		VLGEFVFDKSELNG-VYKATTTTYKLSVGDVFILTSHN				
Human corona 229E pol 1ab (5189)		QMGEEVPEVDYGGDTMTSKSTATTKEVPMLALLSHN				
Murine hepatitis pol 1ab (5578)		VLGEFVFDKSELNG-VYKATTTTYKLSVGDVFILTSHN				
Consensus (5695)		VLGEFVFDKSELNG VYKATTTTYKLSVGDVFILTSHN				
Section 148						
	(5734)	5734	5740	5750	5760	5772
avian infectious bronchitis pol 1ab (5100)		VVSLVAPBCPQOTFSRFVNRNRMVPECEVNTELYH				
bovine coronavirus pol 1ab (5529)		VANTSAPELVLPQE-NYSSIRFASVYSVLETFOQNVVNYQ				
Human corona 229E pol 1ab (5228)		VAPIRPMANCKEYSTIYKEHPSENYSDAANLVRYQ				
Murine hepatitis pol 1ab (5616)		VSSLSAPELVLPQE-NYTSIRFASVYSVPETFOQNVVNYQ				
Consensus (5734)		VASLSAPTLVPQE NYTSIRLASVYSVPETFOQNVVNYQ				
Section 149						
	(5773)	5773	5780	5790	5800	5811
avian infectious bronchitis pol 1ab (5139)		LIVCKKRTLVGGFSGSKSHFAIGLAVYYCTARVVFTAC				
bovine coronavirus pol 1ab (5567)		HIGMRYCTVQGPPTGKSHLAIGLAVYYCTARVVFTAA				
Human corona 229E pol 1ab (5267)		LIVCKKRTLVGGFSGSKSHFAIGLAVYYCTARVVFTAC				
Murine hepatitis pol 1ab (5654)		HIGMRYCTVQGPPTGKSHLAIGLAVYYCTARVVFTAA				
Consensus (5773)		LIGMQRYYTTVQGPPTS GSKSHLAIGLAVYYCTARVVFTAC				
Section 150						
	(5812)	5812	5820	5830	5840	5850
avian infectious bronchitis pol 1ab (5178)		SHAAVDALCEKAHKFELNINDCTRIVPAKVRVDCYSKEFI				
bovine coronavirus pol 1ab (5606)		SHAAVDALCEKAHKFELNINDCTRIVPAKVRVDCYSKEFI				
Human corona 229E pol 1ab (5306)		SHAAVDALCEKAHKFELNINDCTRIVPAKVRVDCYSKEFI				
Murine hepatitis pol 1ab (5693)		SHAAVDALCEKAHKFELNINDCTRIVPAKVRVDCYSKEFI				
Consensus (5812)		SHAAVDALCEKAHKFELNINDCTRIVPAKVRVDCYSKEFI				

FIGURE 4A (contd.)

Section 151					
	(5851)	5851	5860	5870	5889
avian infectious bronchitis pol 1ab (5217)		NDTGKKYVFTSTINALPEVSCATLIVDEVSMLTNYELSVI			
bovine coronavirus pol 1ab (5645)		NDTTRKYVFTSTINALPEMVTQIVVVEVSMLENYELSVI			
Human corona 229E pol 1ab (5345)		NNNSACQYVFTSTINALPEVNADIVVVEVSMLENYELSVI			
Murine hepatitis pol 1ab (5732)		NDTTRKYVFTSTINALPELVTDIVVVEVSMLENYELSVI			
Consensus (5851)		NDTTRKYVFTSTINALPEVVTDIVVVEVSMLENYELSVI			
Section 152					
	(5890)	5890	5900	5910	5928
avian infectious bronchitis pol 1ab (5256)		NCKINHYVYVVDQPAQLPAPRVLISKGTLKPKYFNVT			
bovine coronavirus pol 1ab (5684)		NARIRAKHYVYIGDPAQLPAPRVLISKGTLKPKYFNVT			
Human corona 229E pol 1ab (5384)		NCRISYKHIVYVVDQPAQLPAPRVLISKGTLKPKYFNVT			
Murine hepatitis pol 1ab (5771)		NSRVSARKHYVYIGDPAQLPAPRVLISKGTLKPKYFNVT			
Consensus (5890)		NARISYKHIVYIGDPAQLPAPRVLISKGTLKPKYFNVT			
Section 153					
	(5929)	5929	5940	5950	5967
avian infectious bronchitis pol 1ab (5294)		NLMVGVKLLIPLAKKRCCKKIPDITVMDGCFIANN			
bovine coronavirus pol 1ab (5723)		KLMCCCLGPDIFLGTCYRCPKEIVDTVSALVYENKLRKKN			
Human corona 229E pol 1ab (5423)		QRCACIGUUVFTHKCKIPDITVMDGCFIANN			
Murine hepatitis pol 1ab (5810)		KLMCCCLGPDIFLGTCYRCPKEIVDTVSALVYENKLRKKN			
Consensus (5929)		KLMCCCLGPDIFLGTCYRCPKEIVDTVSALVYENKLRKKN			
Section 154					
	(5968)	5968	5980	5990	6006
avian infectious bronchitis pol 1ab (5333)		PEERECLEIVVNGNSDVGHESGLAYITTOLEEVKDFVC			
bovine coronavirus pol 1ab (5762)		ESSSLCFKVVYKGV---VTTHSSSAVNMQQIHLIKKFLK			
Human corona 229E pol 1ab (5462)		EAKQCTPLFERG---SVQVDNGSINRRRLDVVKRTH			
Murine hepatitis pol 1ab (5849)		DNSSMCKVVYKGV---QTHSSSAVNMQQIHLIKKFLK			
Consensus (5968)		EASSLCFKVVYKGV---VTTHSSSAVNMQQIHLIKKFLK			
Section 155					
	(6007)	6007	6020	6030	6045
avian infectious bronchitis pol 1ab (5372)		RNKQNRRLIPESGSSAMQREYRMELNVOTTESSGGG			
bovine coronavirus pol 1ab (5798)		ANPLAHKVEESPNSQHAARKVLTOTQTVDSAQGSE			
Human corona 229E pol 1ab (5498)		KNSTASKAVTEPYNSQYVAPLGLQTQTVDSAQGSE			
Murine hepatitis pol 1ab (5885)		ANPSWSKAVFISPYNSQNYVAKRVLGLQTQTVDSAQGSE			
Consensus (6007)		ANPSWSKAVFISPYNSQNYVAKRVLGLQTQTVDSAQGSE			
Section 156					
	(6046)	6046	6060	6070	6084
avian infectious bronchitis pol 1ab (5411)		YDYVIESQTADTAHAVNVNRFNVAITRAKKGILCVMSNR			
bovine coronavirus pol 1ab (5837)		YDYVIESQTADTAHAVNVNRFNVAITRAKKGILCVMSNR			
Human corona 229E pol 1ab (5537)		YDYVIESQTADTAHAVNVNRFNVAITRAKKGILCVMSNR			
Murine hepatitis pol 1ab (5924)		YDYVIESQTADTAHAVNVNRFNVAITRAKKGILCVMSNR			
Consensus (6046)		YDYVIESQTADTAHAVNVNRFNVAITRAKKGILCVMSNR			

FIGURE 4A (contd.)

Section 157					
	(6085)	6085	6090	6100	6110 6123
avian infectious bronchitis pol 1ab (5450)		DELYSALKFT	ELDSETS	-----	LQGTGLFNIGNKEES
bovine coronavirus pol 1ab (5876)		QLFEALQFTTL	TLDKVPQAVET	RVQCSTN	LKDCSKSYS
Human corona 229E pol 1ab (5576)		TLEDAKHFET	IMTDLO	-----	SESS-CGLPKDLARNPI
Murine hepatitis pol 1ab (5963)		QLFESLNFTT	TLDKIN	---NPR	LOCTNPKDCSBSYV
Consensus (6085)		QLFEALNFTT	TLDKIN		RLQCSTNLFKDCSKSYS
Section 158					
	(6124)	6124	6130	6140	6150 6162
avian infectious bronchitis pol 1ab (5482)		GVHAYAVTT	KALAAAT	YKVNDEL	ALVNVEAGSETLKN
bovine coronavirus pol 1ab (5915)		GYHPAHAPSE	LAVDDKYKAT	GGDLAVGL	CIGDS-AVTSR
Human corona 229E pol 1ab (5609)		DLPDASHAT	TYLSLSDREKT	SGDCCVQ	GNNN--VCTEH
Murine hepatitis pol 1ab (5999)		GYHPAHAPSE	LAVDDKYKVG	GDVAVCLNV	ADS-AVTSR
Consensus (6124)		GYHPAHAPSE	LALDDKYKVS	GDVAVCLNV	ADS AVTYSR
Section 159					
	(6163)	6163	6170	6180	6190 6201
avian infectious bronchitis pol 1ab (5521)		LISLMGFKL	DVTLDGYH	KLFITRDE	AIKRVAVWGF
bovine coronavirus pol 1ab (5953)		LESDMFKLD	VTLDEYCKL	LITRDE	IKRVAVWGF
Human corona 229E pol 1ab (5646)		MTYMGIRF	DVSMPCSHGL	C.RDFMRH	RGALGMEVE
Murine hepatitis pol 1ab (6037)		LESDMFKLD	VTLDEYCKL	LITRDE	IKRVAVWGF
Consensus (6163)		LISLMGFKL	DVTLDGYH	KLFITRDE	AIKRVAVWGF
Section 160					
	(6202)	6202	6210	6220	6230 6240
avian infectious bronchitis pol 1ab (5560)		GAHATRD	SIGTNFPLQ	LGSTGIDF	VVEPTGLV
bovine coronavirus pol 1ab (5992)		GAHATRD	SIGTNFPLQ	LGSTGIDF	VVEPTGLV
Human corona 229E pol 1ab (5685)		GAHATRD	SIGTNFPLQ	LGSTGIDF	VVEPTGLV
Murine hepatitis pol 1ab (6076)		GAHATRD	SIGTNFPLQ	LGSTGIDF	VVEPTGLV
Consensus (6202)		GAHATRD	SIGTNFPLQ	LGSTGIDF	VVEPTGLV
Section 161					
	(6241)	6241	6250	6260	6279
avian infectious bronchitis pol 1ab (5599)		NEEPVNSK	APGGEQFK	HLIPLMS	RGQPDVVR
bovine coronavirus pol 1ab (6031)		SEKKAVAK	APGGEQFK	HLIPLMS	RGQPDVVR
Human corona 229E pol 1ab (5724)		VVKEVRAR	APGGEQFK	HLIPLMS	RGQPDVVR
Murine hepatitis pol 1ab (6115)		VEKKAAR	APGGEQFK	HLIPLMS	RGQPDVVR
Consensus (6241)		VFKPV	AKAPPGEQ	FKHLIPLMS	RGQPDVVR
Section 162					
	(6280)	6280	6290	6300	6318
avian infectious bronchitis pol 1ab (5638)		ADHLIDLS	DCVVLVT	WAAGLEL	TTLRYFVKIGREV
bovine coronavirus pol 1ab (6070)		ADHLIDLS	DCVVLVT	WAAGLEL	TTLRYFVKIGREV
Human corona 229E pol 1ab (5763)		ADHLIDLS	DCVVLVT	WAAGLEL	TTLRYFVKIGREV
Murine hepatitis pol 1ab (6154)		ADHLIDLS	DCVVLVT	WAAGLEL	TTLRYFVKIGREV
Consensus (6280)		ADHLIDLS	DCVVLVT	WAAGLEL	TTLRYFVKIGREV

FIGURE 4A (contd.)

Section 163						
	(6319)	6319	6330	6340	6357	
avian infectious bronchitis pol 1ab (5676)		EGSRARTEN	SHIQAA	ACWKHC	CGFDEMYN	DLVDIQQW
bovine coronavirus pol 1ab (6109)		CTKRATAY	NCRTGY	YGWRHS	SVTCDYLY	NPLIVDIQQW
Human corona 229E pol 1ab (5801)		CGTVPTCY	NEVSN	DYCGFKH	ALGGCHV	NYMIDLCQW
Murine hepatitis pol 1ab (6193)		CTKRATCEN	NCRTGY	YGWRHS	YSYGUILYN	NPLIVDIQQW
Consensus (6319)		CTKRATCFNS	RRTGYYG	CWKHSLG	CDYLYNPL	IVDIQQW
Section 164						
	(6358)	6358	6370	6380	6396	
avian infectious bronchitis pol 1ab (5715)		YSGNLCFES	DLHONV	HGAHVAS	VUIMTRCL	AINNAFC
bovine coronavirus pol 1ab (6148)		YIOSASSH	LDLYLS	SVHKGAA	VASSDAIM	TRCLAVYDCFC
Human corona 229E pol 1ab (5840)		YVGSISTH	HAHCN	VRNEHVA	SGDAIM	TRCLAVYDCFC
Murine hepatitis pol 1ab (6232)		YTGSLTSN	HDPLCS	SVHKGAA	VASSDAIM	TRCLAVYDCFC
Consensus (6358)		YTGSLSSNH	DLICSVH	KGAHVASS	DAIMTRCL	AVYDCFC
Section 165						
	(6397)	6397	6410	6420	6435	
avian infectious bronchitis pol 1ab (5754)		QDVNLDLT	YPIIAN	DEMSSC	HYLORM	YENACMDALKV
bovine coronavirus pol 1ab (6187)		NNININME	ATISL	LSITSC	VLORVM	LKRAMLCNRY
Human corona 229E pol 1ab (5879)		KNVDLSIT	YPIIAN	ENATIK	GGRTVSH	IMRAIKLYNP
Murine hepatitis pol 1ab (6271)		KSVNINLE	XPIIS	IVSVIT	SCPLL	LRVMFRAAMLCNRY
Consensus (6397)		KNVNWNLT	YPIIAN	ELSIINT	SCRLLQ	RVMLRAAMLCNRY
Section 166						
	(6436)	6436	6450	6460	6474	
avian infectious bronchitis pol 1ab (5793)		NVVYPIQNE	KGI-KC	VRRGDV	NREKNE	IVRVVQFE
bovine coronavirus pol 1ab (6226)		TLCYDINER	---AT	ACVKDF	DEKFEY	DAQIVKSTLL
Human corona 229E pol 1ab (5918)		KAIHDIQNE	---G	IRCAVTD	AWYCKN	INSNMVITL
Murine hepatitis pol 1ab (6310)		DVCYDIGN	PK---G	LACVKC	YDEKFE	QASEVVKSVQFV
Consensus (6436)		VCYDIGNPK		AIACVKDF	DEKFEY	DKNPIVKSVKTL
Section 167						
	(6475)	6475	6480	6490	6500	6513
avian infectious bronchitis pol 1ab (5831)		YDYNQK	DKEDS	ICMIVN	CHVDC	DNSLDTYTNL
bovine coronavirus pol 1ab (6262)		YSEEA	KDSEK	ICMIVN	CHVDC	PNAVCFELV
Human corona 229E pol 1ab (5955)		YDYMTH	G--Q	MLCE	YNCVMT	EFSTYFSTR
Murine hepatitis pol 1ab (6346)		YKYEA	KDQFL	ICMIVN	CHVDC	PNAVCFELV
Consensus (6475)		YDYEAKD		FLDGLCM	FWNCNV	DKYPDNAV
						VCREDTRVL
Section 168						
	(6514)	6514	6520	6530	6540	6552
avian infectious bronchitis pol 1ab (5870)		SVENLP	CGCGS	LYVKNH	YTPKFE	RISERNI
bovine coronavirus pol 1ab (6301)		NNELP	CGCGS	LYVKNH	YTPKFE	RISERNI
Human corona 229E pol 1ab (5992)		STLTP	ERVN	CHVDC	YNCVMT	EFSTYFSTR
Murine hepatitis pol 1ab (6385)		NKLEP	CGCGS	LYVKNH	YTPKFE	RISERNI
Consensus (6514)		S	LNLPGC	NGGS	LYVKNH	AFHTPP
						FDRAAFEN
						LKPMPEF

42/199

FIGURE 4A (contd.)

Section 169					
	(6553)	6553	6560	6570	6580 6591
avian infectious bronchitis pol 1ab (5909)		FEDSSPGETLQVDCGVAQ-	DLVSLATKDCITKCNIGGAVC		
bovine coronavirus pol 1ab (6340)		YYSDFPGVYMDGMDAKQVDYVPLRSATCITKCNIGGAVC			
Human corona 229E pol 1ab (6031)		YDDGSGCEVVDQVN----	YVPLRATNCTKCNIGGAVC		
Murine hepatitis pol 1ab (6424)		YYSDFPGVYMEGMEISKQVDYVPLRSATCITKCNIGGAVC			
Consensus (6553)		YYSDFPGVYMDGMDAKQVDYVPLRSATCITKCNIGGAVC			
Section 170					
	(6592)	6592	6600	6610	6620 6630
avian infectious bronchitis pol 1ab (5947)		KKHAQNTAEFTVTSNAAVTAGCTETWVTNKLNPYNLWKSF			
bovine coronavirus pol 1ab (6379)		LKHAEEYREYLESYNTATTAGCTFWVYKTFDFYNLWNTF			
Human corona 229E pol 1ab (6066)		SKHANLYRAYMEETNIFLQAGFNIVPTTEDCYNILEQTF			
Murine hepatitis pol 1ab (6463)		KKHAEEYREYLESYNTATTAGCTFWVYKTFDFYNLWNTF			
Consensus (6592)		LKHAEEYREYLESYNTATTAGCTFWVYKTFDFYNLWNTF			
Section 171					
	(6631)	6631	6640	6650	6660
avian infectious bronchitis pol 1ab (5986)		SAL--QSIDTAYNMYKGLHYDAIAEMITVITGDAFV			
bovine coronavirus pol 1ab (6418)		TKL--QSLNIVVYNLVKICHYTQQAQEMICALLINDKIVA			
Human corona 229E pol 1ab (6105)		TEVNLGLENIAFVWNKSEVGDGELVATSGDAFV			
Murine hepatitis pol 1ab (6502)		TRL--QSLNIVVYNLVNAGHEDGRAGELCAVIGENVTA			
Consensus (6631)		TKLQSLNIVVYNLVNAGHFDGAGELPCAIIIGDKVVF			
Section 172					
	(6670)	6670	6680	6690	6708
avian infectious bronchitis pol 1ab (6023)		IDQGVKAVFVNQTLRTSVAFELYKKNERTLENRIE			
bovine coronavirus pol 1ab (6455)		KIQKEDVVLIDNNITYFINVAVLEFAKRSIRHHPELKLF			
Human corona 229E pol 1ab (6144)		RDGNTDNLVFNKTSDEININFAFAKRVGLTPLESIT			
Murine hepatitis pol 1ab (6539)		KIQNEDVVVFKNTPFFFINVAVLEFAKRSIRPHPELKLF			
Consensus (6670)		KIQNEDVVVFVNNTTLPINVAVLEFAKRSIRHPELKIL			
Section 173					
	(6709)	6709	6720	6730	6747
avian infectious bronchitis pol 1ab (6062)		KGIGMDVTNGFVTDYANQDELYRNIVKVA--DIEP			
bovine coronavirus pol 1ab (6494)		RNINIDVCMKHITVDARESIFCSNTYGCMTDKEID			
Human corona 229E pol 1ab (6183)		KNICMVATYKFLDQVEAERPLTSFKSVG--DEAE			
Murine hepatitis pol 1ab (6578)		RNINIDVCMGHVLDYAKDSVFCSSKKCKKTDLOCIE			
Consensus (6709)		KNLNIDVTWKHVIWDYAKESPLCSNTYKVCAYTDLDFIE			
Section 174					
	(6748)	6748	6760	6770	6786
avian infectious bronchitis pol 1ab (6099)		NGLVLYDDRYGDYSELADNAFLVSTQCYRYSYMEI			
bovine coronavirus pol 1ab (6533)		KENVLEDGRDNALAEAKRSNCGYISTTKVSLSMIKG			
Human corona 229E pol 1ab (6220)		DVCTCYDNSIQSYERETLSTEALESATAVTGCKS--			
Murine hepatitis pol 1ab (6617)		SENVLEDGRDNALAEAKKCRGMYDNTTKVSLSMIKG			
Consensus (6748)		LNVLFDGRDNGAYEAFKKSNAVYISTTKVKSLSMIKG			

FIGURE 4A (contd.)

Section 175					
	(6787) 6787	6800	6810	6825	
avian infectious bronchitis pol 1ab (6138)	PSNLLVQNGMPLKDGAN	-----	-----	LYVYKRVN-	
bovine coronavirus pol 1ab (6572)	PPRAELNGVVVDKVGDTDCVFEYFAVRKEGQDVIFSO FDS				
Human corona 229E pol 1ab (6257)	LPAIKLNFGMLNGNAIATVKSEDCNIKNINWFMYVEKDC				
Murine hepatitis pol 1ab (6656)	PQRADLNGVVVEKVGDSDVVEEFPAVRKDGDDVIFSPITGS				
Consensus (6787)	PPRADLNGVMVDKVGDSDV	FWFAVRKDGNDVIFSR	DS		
Section 176					
	(6826) 6826	6840	6850	6864	
avian infectious bronchitis pol 1ab (6163)	-----	-----	GAFVTLPTNTINAGRSY		
bovine coronavirus pol 1ab (6611)	L RVSSNQSPQGNLGSNEPCNVGGNDALATSTIFTGSRVIT				
Human corona 229E pol 1ab (6296)	KPVLDHYDG	-----	FMVIGRNLL		
Murine hepatitis pol 1ab (6695)	LEPSSHYSPOGNPGGNRVGDLSGNEALARGTIFTGSRILL				
Consensus (6826)	L VSHY SPQGN G N	G L GNDALA	TIFTQSRLL		
Section 177					
	(6865) 6865	6870	6880	6890	6903
avian infectious bronchitis pol 1ab (6180)	ETTEPRSDIPRDILAMSEESVERIG-KALGLQITLGE				
bovine coronavirus pol 1ab (6650)	SSFTCTDMKKNIALDDDLFTICKLGFEYAFETIVVGIN				
Human corona 229E pol 1ab (6312)	QDLRSTMLEELNMDIGVFIQKYGLFENEEVYVGD				
Murine hepatitis pol 1ab (6734)	SSFTPRSEMHKMDDEDDVFIKYSTQYAFETIVVGS				
Consensus (6865)	SSFTPRSDMEKDFLALDDDDVFIQKYGLDYAFEHIVYGD				
Section 178					
	(6904) 6904	6910	6920	6930	6942
avian infectious bronchitis pol 1ab (6218)	VDKPOEGGATVIGMYLLRANKTNKSVTNSDSCVMQN				
bovine coronavirus pol 1ab (6689)	FNOKIIGGLHLLIGLYRRQOTSNLVIQEFVSYDSSIHSY				
Human corona 229E pol 1ab (6351)	VSKITLGLHLLLSQVFLSKMCIKAEETVAASDITLKC				
Murine hepatitis pol 1ab (6773)	FNOKIIGGLHLLTGHARROOKSNVIOEPYTYDSIHSY				
Consensus (6904)	VNOKIIGGLHLLIGLYRRQQ	SNLVIQEFVSYDSSIHSY			
Section 179					
	(6943) 6943	6950	6960	6970	6981
avian infectious bronchitis pol 1ab (6257)	GFMLSDNG-SYRQVCTVVELLDLDFEELRNLKEYGTN				
bovine coronavirus pol 1ab (6728)	ELTDEKSG-GSKSVCTVIDLLLDLVALVKSLNLCVS-				
Human corona 229E pol 1ab (6390)	CTVTYLNDFSSKLVCTYMEELLDLRSVLRSLDETIVS-				
Murine hepatitis pol 1ab (6812)	ELTDENSG-SKSVCTVIDLLLDLDEVDIMKSLNLCVS-				
Consensus (6943)	FIVDE SG	SSKSVCTVIDLLLDLDFVELLSLNL	CVS		
Section 180					
	(6982) 6982	6990	7000	7010	7020
avian infectious bronchitis pol 1ab (6295)	KSNVVTASIDYHSINEMTNFEDGSIKCTPOTQS--AWT				
bovine coronavirus pol 1ab (6765)	--KVVNVNIDFKDFQFMLWCNDEKVMTFYPRLQAASDWK				
Human corona 229E pol 1ab (6428)	--KYHEVITNKPWRNMLWCKDNAAVAFEGOLDS-AENK				
Murine hepatitis pol 1ab (6849)	--KVVNVNIDFKDFQFMLWCNDEKVMTFYPRLQAADWK				
Consensus (6982)	KVVNVNIDFKDFQFMLWCNDEKVMTFYPRLQAADWK				

FIGURE 4A (contd.)

Section 181					
	(7021)	7021	7030	7040	7059
avian infectious bronchitis pol 1ab (6332)		CGNNP	ELTKVQNCVM	PCNIP	MEVVGELLPSGILMNA
bovine coronavirus pol 1ab (6802)		PGTSM	PLVLYKYLNSPMERVS	SLWNYCKEVTLET	SCMMNVA
Human corona 229E pol 1ab (6464)		CGTSM	GLYNTORMCLEPCNLYN	YGAGIKLPSSGIMFN	VV
Murine hepatitis pol 1ab (6886)		PGYVM	PLVLYKYLESPLE	RVNENNYGKPI	TLTGSCMMNVA
Consensus (7021)		PGYSMP	VLYKYQNSPLER	VNLWNYGKPI	TLPSGIMMNA
Section 182					
	(7060)	7060	7070	7080	7098
avian infectious bronchitis pol 1ab (6371)		KYTQLCQYLSTTTLC	VPHNMRV	LHLGAGSDKG	VAPGSAV
bovine coronavirus pol 1ab (6841)		KYTQLCQYLSTTTLC	VPHNMRV	LHLGAGSDKG	VAPGSAV
Human corona 229E pol 1ab (6503)		KYTQLCQYLSTTTLC	VPHNMRV	LHLGAGSDKG	VAPGSAV
Murine hepatitis pol 1ab (6925)		KYTQLCQYLSTTTLC	VPHNMRV	LHLGAGSDKG	VAPGSAV
Consensus (7060)		KYTQLCQYLSTTTLC	VPHNMRV	LHLGAGSDKG	VAPGSAV
Section 183					
	(7099)	7099	7110	7120	7137
avian infectious bronchitis pol 1ab (6410)		LKQWLPAGTILVDNDVVP	FVSDAVASYFGDCIT	LPFDCQ	
bovine coronavirus pol 1ab (6880)		LKQWLPAGTILVDNDVVP	FVSDAVASYFGDCIT	LPFDCQ	
Human corona 229E pol 1ab (6542)		LKQWLPAGTILVDNDVVP	FVSDAVASYFGDCIT	LPFDCQ	
Murine hepatitis pol 1ab (6964)		LKQWLPAGTILVDNDVVP	FVSDAVASYFGDCIT	LPFDCQ	
Consensus (7099)		LKQWLPAGTILVDNDVVP	FVSDAVASYFGDCIT	LPFDCQ	
Section 184					
	(7138)	7138	7150	7160	7176
avian infectious bronchitis pol 1ab (6449)		FDLIISDNYPITKNIGEYNVSK	----	DGFFTYICHFIK	
bovine coronavirus pol 1ab (6919)		FDLIISDNYPITKNIGEYNVSK	----	DGFFTYICHFIK	
Human corona 229E pol 1ab (6581)		FDLIISDNYPITKNIGEYNVSK	----	DGFFTYICHFIK	
Murine hepatitis pol 1ab (7003)		FDLIISDNYPITKNIGEYNVSK	----	DGFFTYICHFIK	
Consensus (7138)		FDLIISDNYPITKNIGEYNVSK	----	DGFFTYICHFIK	
Section 185					
	(7177)	7177	7190	7200	7215
avian infectious bronchitis pol 1ab (6488)		NNAL	LGGSVAIKITEFSWNAELY	DLMO	KFAFWTMECTNV
bovine coronavirus pol 1ab (6954)		NNAL	LGGSVAIKITEFSWNAELY	DLMO	KFAFWTMECTNV
Human corona 229E pol 1ab (6616)		NNAL	LGGSVAIKITEFSWNAELY	DLMO	KFAFWTMECTNV
Murine hepatitis pol 1ab (7038)		NNAL	LGGSVAIKITEFSWNAELY	DLMO	KFAFWTMECTNV
Consensus (7177)		NNAL	LGGSVAIKITEFSWNAELY	DLMO	KFAFWTMECTNV
Section 186					
	(7216)	7216	7230	7240	7254
avian infectious bronchitis pol 1ab (6527)		NASSE	AFLLIGINYLG	K	KVEIDGNTMHANYLFWRNS
bovine coronavirus pol 1ab (6993)		NASSE	AFLLIGINYLG	K	KVEIDGNTMHANYLFWRNS
Human corona 229E pol 1ab (6655)		NASSE	AFLLIGINYLG	K	KVEIDGNTMHANYLFWRNS
Murine hepatitis pol 1ab (7077)		NASSE	AFLLIGINYLG	K	KVEIDGNTMHANYLFWRNS
Consensus (7216)		NASSE	AFLLIGINYLG	K	KVEIDGNTMHANYLFWRNS

FIGURE 4A (contd.)

						Section 187
	(7255)	7255	7260	7270	7280	7293
avian infectious bronchitis pol 1ab (6565)	NYLQTSAY	SLFDVAKF	DLRLKATP	VVNLKTE	QKTDL	VFN
bovine coronavirus pol 1ab (7030)	TVWNGGAY	SLFDMAFF	PLKLAG	AVENLRAD	QINDM	YS
Human corona 229E pol 1ab (6694)	TVMSLS	SYNSVLLD	LSKENCKH	KATV	VQTKDS	DINEMVLS
Murine hepatitis pol 1ab (7114)	TMWNGGAY	SLFDMSS	PLKAAG	TAVVSI	KPDQIND	DLVLS
Consensus (7255)	TVWNGSAYS	SLFDMAKFP	LKLKATAV	VNLK	DQINDLVLS	
						Section 188
	(7294)	7294	7300	7319		
avian infectious bronchitis pol 1ab (6604)	LIECKGKLL	VRDVGNT	SETSDS	FCYCTM	SEQ ID NO:	9905
bovine coronavirus pol 1ab (7069)	LIEKGGKLL	VRDVGNT	SETSDS	FCYCTM	SEQ ID NO:	9886
Human corona 229E pol 1ab (6733)	LVRSEKLL	VRGNGK	CLSF	SNHEWSTK	SEQ ID NO:	9914
Murine hepatitis pol 1ab (7153)	LIEKGGKLL	VRDVGNT	SETSDS	FCYCTM	SEQ ID NO:	9887
Consensus (7294)	LIEKGGKLL	VRDVGNT	SETSDS	FCYCTM		

FIGURE 4B

		Section 1				
		(1)	1	10	20	39
human coronavirus OC43 NP	(1)	MSFTPGKQSSS-RASSGNRSGNGILK---WADQSDQVRN				
Bovine corona NP	(1)	MSFTPGKQSSS-RASFGNRSGNCLLK---WADQSDQSRN				
avian infectious bronchitis virus NP	(1)	-----MASSKAAG--KSSSP--AP-				
mouse hepatitis virus NP	(1)	MSFVPGQENAGGRSSSVNRAGNCLLKTTWADQTERGPN				
Consensus	(1)	MSFTPGKQSSS RASSGNRSGNGILK WADQSDQARN				
		Section 2				
		(40)	40	50	60	78
human coronavirus OC43 NP	(36)	VQTRGRRAQPKQTATSQPSGGNVVPPYYSWFSGITQFQK				
Bovine corona NP	(36)	VQTRGRRAQPKQTATSQPSGGNVVPPYYSWFSGITQFQK				
avian infectious bronchitis virus NP	(16)	IKLGGPKPKLVGSSGN-----ASNEQATKAKKL				
mouse hepatitis virus NP	(40)	NONRRRNQKQTATIQ-PNSGSSVDPHYYSWFSGITQFQK				
Consensus	(40)	VQTRGRRAQPKQTATSQ PSGGNVVPPYYSWFSGITQFQK				
		Section 3				
		(79)	79	90	100	117
human coronavirus OC43 NP	(75)	GKEEEFVHOCPVTIAPGVPAATEAKYVYHNRSRTAD				
Bovine corona NP	(75)	GKEEEFAQCVTIAPGVPAATEAKYVYHNRSRTAD				
avian infectious bronchitis virus NP	(45)	NAPAPKFLQSEVDNENDKNSQCHVNRQA--KPGK				
mouse hepatitis virus NP	(78)	GKEEFQATQCVTIANGIPASBOKYVYHNRSRTAD				
Consensus	(79)	GKEFEFAEGQGVPPIAPGVPAASEQKGYWRHNRRSFKTAD				
		Section 4				
		(118)	118	130	140	156
human coronavirus OC43 NP	(114)	GNORQLLPRWYFYLLGTGPHAKDOYTDIDVEVANSQ				
Bovine corona NP	(114)	GNORQLLPRWYFYLLGTGPHAKDOYTDIDVEVANSQ				
avian infectious bronchitis virus NP	(82)	GGRKPMPDALVYTTTAAADLNWDSQDILVAKG				
mouse hepatitis virus NP	(117)	QOKODLPRWYFYLLGTGPHAKDOYTDIDVEVANSQ				
Consensus	(118)	GNQKQLLPRWYFYLLGTGPHAKDOYGTSIDGVFWVASNQ				
		Section 5				
		(157)	157	170	180	195
human coronavirus OC43 NP	(153)	ADVNTPADIVDRDPSSDEAIPTRFPPG---TVLPQGGYYI				
Bovine corona NP	(153)	ADVNTPADILDSSDEAIPTRFPPG---TVLPQGGYYI				
avian infectious bronchitis virus NP	(121)	AVKSRSNQGTEDENFDQYLRSSDEGPDGNFRWDEIP				
mouse hepatitis virus NP	(156)	ADVNTSRDLVESSDEAIPTRFPPG---TVLPQGGYYI				
Consensus	(157)	ADVNTRADIVDRDPSSDEAIPTRFPPG TVLPQGGYYI				
		Section 6				
		(196)	196	210	220	234
human coronavirus OC43 NP	(189)	EGSGRSAPNSRSTSRASSRASSAGSRSRANSNGNRTPTSG				
Bovine corona NP	(189)	EGSGRSAPNSRSTSRASSRASSAGSRSRANSNGNRTPTSG				
avian infectious bronchitis virus NP	(160)	LSRGRSTAASAASEVPSR-----EGSGRRG				
mouse hepatitis virus NP	(192)	EGSGRSAPASRSGRSRSGPNN--RASSSNQQAAT				
Consensus	(196)	EGSGRSAPNSRSTSRASSRASSAGSRSRANSNGNRTPTSG				

FIGURE 4B (contd.)

Section 7																																						
	(235)	235	240	250	260	273																																
human coronavirus OC43 NP (228)		VT	PD	MA	DQ	IASLVLAKLGKDATKPGQVTFHFAKEVROKI																																
Bovine corona NP (228)		VT	PD	MA	DQ	IASLVLAKLGKDATKPGQVTFKOTAKEIROKI																																
avian infectious bronchitis virus NP (192)		A	E	D	L	IARAAPITQDQQ----RKGTPTTKQAEEMAHRR																																
mouse hepatitis virus NP (229)		V	K	P	Q	MAEELMALVLAKLGKDAQGPQVTKQSKVROKI																																
Consensus (235)		V	T	P	D	MA	DQ	IASLVLAKLGKDATKPGQVTFKOTAKEVROKI																														
Section 8																																						
	(274)	274	280	290	300	312																																
human coronavirus OC43 NP (267)		L	N	K	P	RQKSPNKQCTVQCCFGKRGPNQ--HFGGGEMLKL																																
Bovine corona NP (267)		L	N	K	P	RQKSPNKQCTVQCCFGKRGPNQ--HFGGGEMLKL																																
avian infectious bronchitis virus NP (227)		E	C	K	---	KTVPPGYRDCVTCPTKGGEGNEGDDKNEE																																
mouse hepatitis virus NP (268)		L	N	K	P	RQKSPNKQCTVQCCFGKRGPNQ--HFGGGEMLKL																																
Consensus (274)		L	N	K	P	RQKSPNKQCTVQCCFGKRGPNQ	NFGGGEMLKL																															
Section 9																																						
	(313)	313	320	330	340	351																																
human coronavirus OC43 NP (304)		G	T	S	D	PQFPILAEIAPTAGAFFFSRLELAKVON-----																																
Bovine corona NP (304)		G	T	S	D	PQFPILAEIAPTAGAFFFSRLELAKVON-----																																
avian infectious bronchitis virus NP (262)		G	I	K	D	G	R	V	T	A	M	L	N	I	T	S	P	H	A	C	L	T	G	R	V	T	P	K	L	O	P	D	G	L	H	L	R	F
mouse hepatitis virus NP (305)		G	T	S	D	PQFPILAEIAPTAGAFFFSRLELAKVON-----																																
Consensus (313)		G	T	S	D	PQFPILAEIAPTAGAFFFSRLELAKVON																																
Section 10																																						
	(352)	352	360	370	380	390																																
human coronavirus OC43 NP (337)		---	L	S	G	N	P	D	E	P	O	K	D	V	Y	E	L	R	N	G	A	I	R	D	S	T	L	S	G	E	E	T	I	M	K	V		
Bovine corona NP (337)		---	L	S	G	N	L	L	E	P	O	K	D	V	Y	E	L	R	N	G	A	I	R	D	S	T	L	S	G	E	E	T	I	M	K	V		
avian infectious bronchitis virus NP (301)		E	F	T	T	V	V	P	R	D	I	O	F	I	N	V	K	I	C	D	E	C	M	D	G	V	C	R	P	K	D	E	V	M	R	P	K	
mouse hepatitis virus NP (337)		---	S	G	A	D	E	P	T	K	D	V	Y	E	L	O	X	S	G	A	V	R	E	D	S	T	L	S	G	E	E	T	I	M	K	V		
Consensus (352)		---	L	S	G	N	P	D	E	P	O	K	D	V	Y	E	L	R	N	G	A	I	R	D	S	T	L	S	G	E	E	T	I	M	K	V		
Section 11																																						
	(391)	391	400	410	429																																	
human coronavirus OC43 NP (373)		L	N	E	N	L	N	A	Y	Q	Q	D	G	M	M	N	S	P	K	P	O	R	G	H	K	N	G	Q	---	G	E	N	D	N				
Bovine corona NP (373)		L	N	E	N	L	N	A	Y	Q	Q	D	G	M	M	N	S	P	K	P	O	R	G	O	R	N	G	Q	---	G	E	N	D	N				
avian infectious bronchitis virus NP (340)		S	R	P	S	---	R	P	A	T	R	T	S	S	P	A	P	R	O	P	O	K	K	E	K	S	E	---	K	O	D	D	E					
mouse hepatitis virus NP (372)		L	N	E	N	L	N	A	Y	Q	Q	D	G	A	D	V	S	T	K	P	O	---	K	G	R	R	O	A	O	E	K	K	D	E	V	N		
Consensus (391)		L	N	E	N	L	N	A	Y	Q	Q	D	G	M	M	N	S	P	K	P	O	R	G	K	N	G	Q	---	G	E	N	D	N					
Section 12																																						
	(430)	430	440	450	468																																	
human coronavirus OC43 NP (409)		I	S	V	A	P	K	S	R	V	Q	Q	N	K	S	R	E	L	T	A	E	D	I	S	L	L	K	K	M	D	D	P	---	Y	T			
Bovine corona NP (409)		I	S	V	A	P	K	S	R	V	Q	Q	N	K	S	R	E	L	T	A	E	D	I	S	L	L	K	K	M	D	D	P	---	Y	T			
avian infectious bronchitis virus NP (373)		M	D	K	A	L	T	S	D	E	E	R	N	---	A	O	L	E	F	D	E	P	K	V	I	N	W	G	D	S	---	---	A					
mouse hepatitis virus NP (410)		M	S	V	A	K	E	K	S	S	M	O	R	N	V	S	R	E	L	T	P	E	D	R	S	L	L	A	O	L	D	G	V	V	P	D	G	L
Consensus (430)		I	S	V	A	P	K	S	R	V	Q	Q	N	K	S	R	E	L	T	A	E	D	I	S	L	L	K	K	M	D	D	P	---	Y	T			
Section 13																																						
	(469)	469	474																																			
human coronavirus OC43 NP (443)		E	D	T	S	E	I	SEQ ID NO: 9915																														
Bovine corona NP (443)		E	D	T	S	E	I	SEQ ID NO: 9887																														
avian infectious bronchitis virus NP (404)		L	G	E	N	E	L	SEQ ID NO: 9906																														
mouse hepatitis virus NP (449)		E	D	D	S	N	M	SEQ ID NO: 9898																														
Consensus (469)		E	D	T	S	E	I																															

FIGURE 4C

Section 1						
	(1)	10	20	30	42	
human coronavirus OC43 HE	(1)	----MFLLEPRFILV	SCIIGSLGTYNRRTNVV	LVNGENEELFG		
bovine coronavirus HE	(1)	----MFILLRREVLV	SCIIGSLGEDNPPTNVV	SHLNGEWFLEQ		
mouse hepatitis virus HE	(1)	MARTDAMAEPTLE	HLVLSLGYAFGENEEL	LVVSHLNDDELEFG		
Consensus	(1)	MFLLEPRFILV	SCIIGSLGFFNPPTNVV	SHLNGDWELFG		
Section 2						
	(43)	43	50	60	70	84
human coronavirus OC43 HE	(39)	DSRSDCNHIVNINP	NYSYMDLNPVLCDSG	KISSKAGNSIFR		
bovine coronavirus HE	(39)	DSRSDCNHVVNTN	PRNYSYMDENPALC	DSGKISSKAGNSIFR		
mouse hepatitis virus HE	(43)	DSRSDCNHINNLS	QQNANYHDIPELCK	SAKISATAENSELEK		
Consensus	(43)	DSRSDCNHIVNINP	NYSYMDLNP	LCDSGKISSKAGNSIFR		
Section 3						
	(85)	85	90	100	110	126
human coronavirus OC43 HE	(81)	SEHETDFYNVYCE	GOITFTIGGVETRY	HAEGNRSC	SGNDIW	
bovine coronavirus HE	(81)	SEHETDFYRYTCE	GOITFTYGLNFTTH	AFGTTS	SGNDIW	
mouse hepatitis virus HE	(85)	SEHETDFYNYCE	GOITFTIGGVETRY	HAEGNRSC	SGNDIW	
Consensus	(85)	SEHETDFYNYTGE	GQQIIFYEGVNETPY	HAFKSGSNDIW		
Section 4						
	(127)	127	140	150	168	
human coronavirus OC43 HE	(123)	MQNKGLFYTQVYKN	MAVYRSLTFVNVPY	VYNGSAQSTALCKS		
bovine coronavirus HE	(123)	MQNKGLFYTQVYKN	MAVYRSLTFVNVPY	VYNGSAQSTALCKS		
mouse hepatitis virus HE	(127)	MGNKARFYTQVYKN	MAHYRSLSVLNTFT	TYNGVAGVSMGRH		
Consensus	(127)	MQNKGLFYTQVYKN	MAVYRSLTFVNVPY	VYNGSAQSTALCKS		
Section 5						
	(169)	169	180	190	200	210
human coronavirus OC43 HE	(165)	GS----LVLNNTAY	IAPQANSGLVYAKV	EADFYLSGDEYIV		
bovine coronavirus HE	(165)	GS----LVLNNTAY	IAREANFGDLVYKV	EADFYLSGDEYIV		
mouse hepatitis virus HE	(169)	IANGVTITLNTTET	ICKEVSKPTVYVES	SEANTLOCGDEIV		
Consensus	(169)	GS	LVLNNTAYIAKEAN	GDYYYKVEADFYLSG	DEYIV	
Section 6						
	(211)	211	220	230	240	252
human coronavirus OC43 HE	(203)	PLCIFNGKFLSNTK	YDDSQYYFNKDTG	VIYGLNSTETITTG		
bovine coronavirus HE	(203)	PLCIFNGKFLSNTK	YDDSQYYFNKDTG	VIYGLNSTETITTG		
mouse hepatitis virus HE	(211)	PLCIFNGKFLSNTK	YDDSQYYFNKDTG	VIYGLNSTETITTG		
Consensus	(211)	PLCIFNGKFLSNTK	YDDSQYYFNKDTG	VIYGLNSTETITTG		
Section 7						
	(253)	253	260	270	280	294
human coronavirus OC43 HE	(245)	EDLNCHYLVLP	SGNYLAISNELLLTV	PTKAICLNKRKDFTPV		
bovine coronavirus HE	(245)	EDPNCHYLVLP	SGNYLAISNELLLTV	PTKAICLNKRKDFTPV		
mouse hepatitis virus HE	(253)	LDFTCIYVA	TPGNYLS	ANFLLVYSKAGLER	PPAL	LV
Consensus	(253)	FDLNCHYLVLP	SGNYLAISNELLLTV	PTKAICLNKRKDFTPV		

49/199

FIGURE 4C (contd.)

Section 8						
	(295)	295	300	310	320	336
human coronavirus OC43 HE (287)		QVVD	SRWNNARQSDNMTAVACQPPYCYFRNSTTNYVGVYDIN			
bovine coronavirus HE (287)		QVVD	SRWNNARQSDNMTAVACQPPYCYFRNSTTNYVGVYDIN			
mouse hepatitis virus HE (295)		QVVD	SRWNNARQSDNMTAVACQPPYCYFRNSTTNYVGVYDIN			
Consensus (295)		QVVD	SRWNNARQSDNMTAVACQPPYCYFRNSTTNYVGVYDIN			
Section 9						
	(337)	337	350	360	378	
human coronavirus OC43 HE (329)		HGDAGFTSILSGLLYNSPCFSQQGVFRYDNVSSVWPLYPYGR				
bovine coronavirus HE (329)		HGDAGFTSILSGLLYNSPCFSQQGVFRYDNVSSVWPLYPYGR				
mouse hepatitis virus HE (337)		HGDAGFTSILSGLLYNSPCFSQQGVFRYDNVSSVWPLYPYGR				
Consensus (337)		HGDAGFTSILSGLLYNSPCFSQQGVFRYDNVSSVWPLYPYGR				
Section 10						
	(379)	379	390	400	410	420
human coronavirus OC43 HE (371)		CPTAADINPDLPICVYDPLPVILLGILLGVAVIIIVVLLLY				
bovine coronavirus HE (371)		CPTAADINPDLPICVYDPLPVILLGILLGVAVIIIVVLLLY				
mouse hepatitis virus HE (379)		CPTAADINPDLPICVYDPLPVILLGILLGVAVIIIVVLLLY				
Consensus (379)		CPTAADINPDLPICVYDPLPVILLGILLGVAVIIIVVLLLY				
Section 11						
	(421)	421	432			
human coronavirus OC43 HE (413)		FMVDNGTRLHDA		SEQ ID NO: 9916		
bovine coronavirus HE (413)		FMVDNGTRLHDA		SEQ ID NO: 9888		
mouse hepatitis virus HE (420)		FMVDNGTRLHDA		SEQ ID NO: 9899		
Consensus (421)		FMVDNGTRLHDA				

FIGURE 4D

Section 1					
	(1)	1	10	20	39
bovine coronavirus Sm	(1)	MFMA	AAAFADTVWYVGQIIFIVAICLLVII	--	VVVAFLA
avian infectious bronchitis virus Sm	(1)	MNLL	NKSLEEENGSELTAYIIVGFLAYILLGRALQ		IVQ
mouse hepatitis virus Sm	(1)	--MF	NLEITDTVWYVGQIIFIVAICLLVII	--	IVVFLA
Consensus	(1)	M M N	FL DTVWYVGQIIFIVAICLLVII		IVVAFLA
Section 2					
	(40)	40	50	60	78
bovine coronavirus Sm	(38)	IFKLC	IQLCGLCNTLVLSPSIYLF R KQ YKFYN ELK		
avian infectious bronchitis virus Sm	(40)	AADA	ACLEWYTWVHPGAKGTAFVYKTYGRKLN		PEBE
mouse hepatitis virus Sm	(36)	SIKLC	IQLCGLCNTLVLSPSIYLF R KQ YKFYN ELK		
Consensus	(40)	S KLC	IQLCGLCNTLVLSPSIYLF R KQ YKFYN ELK		
Section 3					
	(79)	79	90	108	
bovine coronavirus Sm	(76)	PPVLDVDDI			SEQ ID NO: 9889
avian infectious bronchitis virus Sm	(79)	AVIVNEFPKNGWNNKNPANFQDAQRDKLYS			SEQ ID NO: 9907
mouse hepatitis virus Sm	(75)	LPVLDVDDI			SEQ ID NO: 9900
Consensus	(79)	PILDVDDI			

FIGURE 4E

		Section 1				
		(1)	10	20	30	40
human coronavirus OC43 M	(1)	-MSSKTPAPVYIWTADEAIFKFLKEWNFSLGIILLFITII				
bovine coronavirus M	(1)	-MSSVITTPAPVYIWTADEAIFKFLKEWNFSEGLITILLFIILLI				
avian infectious bronchitis virus M	(1)	-----MSNAANCTLDCEQSVLEFLEKFLFITAFLLFTILB				
mouse hepatitis virus M	(1)	MTSTTQAPQPVYQWTADEAIFKFLKEWNFSLGITILLFVILLI				
Consensus	(1)	MSS TTPAPVYIWTADEAIFKFLKEWNFSLGIILLFITII				
		Section 2				
		(41)	41	50	60	70
human coronavirus OC43 M	(40)	LLEFYPSRSMFVYVIIMTLEWLMARLTILLITIFNCVYALN				
bovine coronavirus M	(40)	LLEFYTSIMFVYVIKMIILKLMARLTILLITIFNCVYALN				
avian infectious bronchitis virus M	(36)	LQYIATSRRTFMNIVLWCFWELNIAMGVISCTPPN				
mouse hepatitis virus M	(41)	LLEFYPSRSMFVYVVKMIILKLMARLTILLITIFNCVYALN				
Consensus	(41)	LQFGYTSRSMFVYVIKMIILWLMWPLTIILTIFNCVYALN				
		Section 3				
		(81)	81	90	100	110
human coronavirus OC43 M	(80)	NVYLGSLVFTIVAIMWIVFVNSIRLFIRTGSWWSFNP				
bovine coronavirus M	(80)	NVYLGSLVFTIVAIMWIVFVNSIRLFIRTGSWWSFNP				
avian infectious bronchitis virus M	(76)	TGGIVAAKILLVACLSEEGWIOQLREPKGQWAAK				
mouse hepatitis virus M	(81)	NVYLGSLVFTIVAIMWIVFVNSIRLFIRTGSWWSFNP				
Consensus	(81)	NVYLGSLVFTIVAIMWIVFVNSIRLFIRTGSWWSFNP				
		Section 4				
		(121)	121	130	140	150
human coronavirus OC43 M	(120)	ETNNLMCIDMKGTMYVRPIIEDYHTLTVTIIRGHLYMQGI				
bovine coronavirus M	(120)	ETNNLMCIDMKGRMSVRPIIEDYHTLTVTIIRGHLYMQGI				
avian infectious bronchitis virus M	(116)	ESIAVGSLLDSNGQOCNFALESVPMLSLFLIKNGVLYCEG				
mouse hepatitis virus M	(121)	ETNNLMCIDMKGTMYVRPIIEDYHTLTVTIIRGHLYMQGI				
Consensus	(121)	ETNNLMCIDMKGTMYVRPIIEDYHTLTVTIIRGHLYMQGI				
		Section 5				
		(161)	161	170	180	190
human coronavirus OC43 M	(160)	KLGTGYSWADLPAYMTAKVTHLCTYKRGFLDKIDTSGE				
bovine coronavirus M	(160)	KLGTGYSLSDLPAYVTAKVSHLCTYKRGFLDKIDTSGE				
avian infectious bronchitis virus M	(156)	QWLAKCEPDHLEKDTIFMCPDGRNIR-----MV				
mouse hepatitis virus M	(161)	KLGTGYSLSDLPAYVTAKVSHLCTYKRGFLDKIDTSGE				
Consensus	(161)	KLGTGYSLSDLPAYVTAKVSHLCTYKRGFLDKIDTSGE				
		Section 6				
		(201)	201	210	220	230
human coronavirus OC43 M	(200)	AVYVKSQVGNRYRLPSTQKSGMDTALLRNNI				
bovine coronavirus M	(200)	AVYVKSQVGNRYRLPSTQKSGMDTALLRNNI				
avian infectious bronchitis virus M	(185)	QKVTGDSQSNKKRFAT-----				
mouse hepatitis virus M	(201)	AVYVKSQVGNRYRLPSN-KPSGMDTALLRNI				
Consensus	(201)	AVYVKSQVGNRYRLPSTQKSGMDTALLRNNI				

SEQ ID NO: 9917
 SEQ ID NO: 9890
 SEQ ID NO: 9908
 SEQ ID NO: 9901

51/199

FIGURE 4F

Section 1						
	(1)	10	20	30	40	
human coronavirus OC43 S	(1)	MELILLISLPTAF	AVIGDLKCTSDN	INDPKDTGPP	PTSTTD	
avianinfectiousbronchitisvirusS	(1)	-----	-----	-----	-----	
bovine coronavirus S	(1)	MELILLISLPTAF	AVIGDLKCTTVS	INDVDTGVP	PSISTD	
mouse hepatitis virus S	(1)	MLEMFLFLFPS	CIIGYIGDFRCICLVNSNGANVFAP	STSTSE		
Consensus	(1)	MELILLISLPTAF	AVIGDLKCTSL	IND DTG	PSISTD	
Section 2						
	(41)	41	50	60	70	80
human coronavirus OC43 S	(40)	TVDVTNGLGTY	YVLD	RVYLN	TTL	LLNGYPTSGSTYRNMA
avianinfectiousbronchitisvirusS	(1)	-----	-----	-----	-----	-----
bovine coronavirus S	(40)	TVDVTNGLGTY	YVLD	RVYLN	TTL	LLNGYPTSGSTYRNMA
mouse hepatitis virus S	(41)	TVEVSQGLGTY	YVLD	RVYLN	ATL	LLTTCGYYPVDGSKFRNDA
Consensus	(41)	TVDVTNGLGTY	YVLD	RVYLN	TTL	LLNGYPTSGSTYRNMA
Section 3						
	(81)	81	90	100	110	120
human coronavirus OC43 S	(80)	LKGSVLLSRLW	KPEFLS	DFINGIEAK	VKN	TKVTKDRVMY
avianinfectiousbronchitisvirusS	(23)	SSSYVYYYQSA	ERISG	WHLQGLAM	VENIS	SEFNNAGSS
bovine coronavirus S	(80)	LKGTLLLSLTL	WKEPEFLS	DFRTNIEAK	VKN	TKVTKDGVMY
mouse hepatitis virus S	(81)	LTGTNSVLSL	SWTQSEYLS	QENDCTFAK	VON	LKTSTPSGAT
Consensus	(81)	LKGTVLLS	SWFKPPFLS	DFNNGIFAK	VKN	TKVIKDAVMY
Section 4						
	(121)	121	130	140	150	160
human coronavirus OC43 S	(120)	SEFPATITIG	SSTFVNTS	YSV	VVQ	PERTINSTQDGNKLGGL
avianinfectiousbronchitisvirusS	(63)	SGCTVGITH	HGGRV	VNASS	IAMTAP	-----S-----
bovine coronavirus S	(120)	SEFPATITIG	SSTFVNTS	YSV	VVQ	PERTINSTQDGNKLGGL
mouse hepatitis virus S	(121)	AYEPPIVIG	SLGEGYTS	ETVV	EE	-----YNG-----VT
Consensus	(121)	SEFPATITIG	SSTFVNTS	YSV	VVQ	P T GNKLQGLL
Section 5						
	(161)	161	170	180	190	200
human coronavirus OC43 S	(160)	EVSVCOYNMCE	YPOTTCHPNLG	NHRKEL	WHLD	DTGVVVSCL
avianinfectiousbronchitisvirusS	(88)	--GMAWSSS	ECTAH	NFS	DTTVFVTHC	MKHGGCPLTGM
bovine coronavirus S	(156)	EVSVCOYTMCE	YPNTTICNPNLG	NQRMEL	WHWD	DTGVVVSCL
mouse hepatitis virus S	(149)	MAVCOYTI	ICLLPYTDCKPNT	NGNKLIG	WHTE	DKPPICV
Consensus	(161)	EISVCOYTMCE	YPNTTICNPNLG	N RIELWH	DTGVV	SCL
Section 6						
	(201)	201	210	220	230	240
human coronavirus OC43 S	(199)	MKRNETYDVN	ADYLYFHFYQ	EGGTEYAY	FTDT	GVVTKFLF
avianinfectiousbronchitisvirusS	(126)	LQONLIRVS	AMNGQLF	NLT	VSVAKYPT	ERSFQCVNNIT
bovine coronavirus S	(195)	MKRNETYDVN	ADYLYFHFYQ	EGGTEYAY	FTDT	GVVTKFLF
mouse hepatitis virus S	(189)	LKRFTLN	YNADAFYFHFYQ	HGGTEYAY	ADKPSA	TEFLF
Consensus	(201)	MKRNETYDVN	ADYLYFHFYQ	EGGTEYAY	FTDT	GVVTKFLF

FIGURE 4F (contd.)

Section 7						
	(241)	241	250	260	270	280
human coronavirus OC43 S	(239)	NVYLGMALSHYYVMPLTCN----	SKLTLEYWVTPLTSSROY			
avianinfectiousbronchitisvirusS	(166)	SVYLDNGDLYVTSNETLIDVTSAGVYFKAGGPITYKVMREVK				
bovine coronavirus S	(235)	NVYLGLTVMLSHYYVMPLTCN----	SALTLEYWVTPLTSSROY			
mouse hepatitis virus S	(229)	SVYLDGDLITLQYVLEPTICNPTAGSTFAPRYWVTPLTSSROY				
Consensus	(241)	SVYLGILSHYYVMPLTCN	A	S	LTLEYWVTPLTSSROY	
Section 8						
	(281)	281	290	300	310	320
human coronavirus OC43 S	(275)	LLAFNQDDHFFENAEDCMSDFMSEIKCKTQSIAPSTGVYEL				
avianinfectiousbronchitisvirusS	(206)	ALAYFVNQTAQDVLLDCSPRGLHACQYNTGNFSDGFPE				
bovine coronavirus S	(271)	LLAFNQDGVIFNAVDCKSDFMSEIKCKTILSIAPSTGVYEL				
mouse hepatitis virus S	(269)	LFNENQKGVITSAVDCASSYTSEIKCKTOSMLRSTOVLE				
Consensus	(281)	LLAFNQDGVIFNAVDC	SSFMSEIKCKTQSIAPSTGVYEL			
Section 9						
	(321)	321	330	340	350	360
human coronavirus OC43 S	(315)	NGYTVQPIADVYRRKPNLPCNIEAWLNDKSVPSPLNWER				
avianinfectiousbronchitisvirusS	(246)	TNSSLVKQKFFVYN-----	NSVMNTTCTLHNFIEHN			
bovine coronavirus S	(311)	NGYTVQPIADVYRRKPNLPCNIEAWLNDKSVPSPLNWER				
mouse hepatitis virus S	(309)	SGYTVQPVGVYRRVANLPACNIEAWLTARSVPSPINWER				
Consensus	(321)	NGYTVQPIADVYRRIPNLP	CNIEAWLNDKSVPSPLNWER			
Section 10						
	(361)	361	370	380	390	400
human coronavirus OC43 S	(355)	KTFSSNCNFMSSSLMSFIQADSETCNNIDAAKIYGMCFSSI				
avianinfectiousbronchitisvirusS	(277)	ELGAPNP-----	SGVNIQTYQTKTAOSGYNNFNSEF			
bovine coronavirus S	(351)	KTFSSNCNFMSSSLMSFIQAYSETCNNIDAAKIYGMCFSSI				
mouse hepatitis virus S	(349)	KTFSSNCNFMSSSLIRYVAESLFCNNIDAASKVYGRCEGSE				
Consensus	(361)	KTFSSNCNFMSSSLMSFIQADSETCNNIDAAKIYGMCFSSI				
Section 11						
	(401)	401	410	420	430	440
human coronavirus OC43 S	(395)	TIDKFAIPNGRKVDLQGLNLGYLQSFNYRIDTTATSCQLY				
avianinfectiousbronchitisvirusS	(311)	SSFVYKESNFMYGSHPSCKFRETTINGELWFNSLSVSHA				
bovine coronavirus S	(391)	TIDKFAIPNGRKVDLQGLNLGYLQSFNYRIDTTATSCQLY				
mouse hepatitis virus S	(389)	SYDKFAVPPSRQVDLQGLNSGFLQTAHYRIDTAATSCQLH				
Consensus	(401)	SIDKFAIPNGRKVDLQGLNLGYLQSFNYRIDTTATSCQLY				
Section 12						
	(441)	441	450	460	470	480
human coronavirus OC43 S	(435)	YNLPAANVSVSRRFPSTWNRREGFIEDSVFKPNPAGVLTN				
avianinfectiousbronchitisvirusS	(351)	YGP-----	LOG-----			
bovine coronavirus S	(431)	YNLPAANVSVSRRFPSTWNRREGFETOSVEKPNPAGVFTD				
mouse hepatitis virus S	(429)	YTLPKNNVTINNNHNPSSWNRRYGENDAGVEGKN-----	Q			
Consensus	(441)	YNLPAANVSVSRRFPSTWNRREGF	E	SVFKPNPAGV	TN	

FIGURE 4F (contd.)

Section 13						
	(481)	481	490	500	510 520	
human coronavirus OC43 S	(475)	HDVVYAQHCEKAPKNEEPCKLNG-SCVGS	GP-----	GKNN		
avianinfectiousbronchitisvirusS	(357)	---GCKQSVFKGRATCCYAYS	YGGPSLCKGV	YSG-----		
bovine coronavirus S	(471)	HDVVYAQHCEKASINFCPC	KUDGSLCVGNGPG	IDAGYKTS		
mouse hepatitis virus S	(463)	HDVVYAQCGTIVRSYYCPCA	QPDIMSPCIT	QTQK-----	P	
Consensus	(481)	HDVVYAQHCEKARSNFC	PCKL G LSVGS	GP	K	
Section 14						
	(521)	521	530	540	550 560	
human coronavirus OC43 S	(509)	GIGTC	PAGTNYLTCDN-----	LCTPD	PIIT--FTGT	YKCP
avianinfectiousbronchitisvirusS	(388)	-----	-----	-----	-----	
bovine coronavirus S	(511)	GIGTC	PAGTNNLTCHNAAQCDC	LCTPD	PIITSKAT	G
mouse hepatitis virus S	(497)	-----	-----	-----	-----	
Consensus	(521)	GIGTC	PAGTNYLTC N	LCTPD	PIIT	TG YKCP
Section 15						
	(561)	561	570	580	590 600	
human coronavirus OC43 S	(541)	QTKSLV	GIGEHSGIAVKS	DYCG-----	GNSCTCR	POAFLG
avianinfectiousbronchitisvirusS	(388)	----EILD	HNFEGLEVVY	TKSGG-----	-----	
bovine coronavirus S	(551)	QTKYLV	GIGEHSGIAVKS	DHCG-----	GNPCTC	QPOAFLG
mouse hepatitis virus S	(497)	-KSAFMV	VGDHCEGEGVLE	DCCGNAD	PHKGCICANN	SFLG
Consensus	(561)	QTKALV	GIGEHCSGLAVKS	DHCG	GN CTC	POAFLG
Section 16						
	(601)	601	610	620	630 640	
human coronavirus OC43 S	(577)	WSADSC	LOGDRCNIFANFILH	DVNSGLT	CTSTD	LQKANTDI
avianinfectiousbronchitisvirusS	(407)	-----	-----	SR-	LOTATE	PEFVITANNYNN
bovine coronavirus S	(587)	WSVDSC	LOGDRCNIFANFILH	DVNSGLT	CTSTD	LQKANTDI
mouse hepatitis virus S	(536)	WSHDTCL	VNDRCQITANILL	NGINS	SGTTC	STD
Consensus	(601)	WS	DSCLQGDRCNIFANFILH	DINS	SGTTC	STD
Section 17						
	(641)	641	650	660	670 680	
human coronavirus OC43 S	(617)	ILGV	CVNYDLYGILGCGIT	VEVNATYYNS	WQNL	LYDSNGN
avianinfectiousbronchitisvirusS	(427)	TENT	CVNDNNITGRTGQ	FTIN	YTD	SAVS--YNYLA
bovine coronavirus S	(627)	ILGV	CVNYDLYGILGCGIT	VEVNATYYNS	WQNL	LYDSNGN
mouse hepatitis virus S	(576)	VTGHC	YKYDLYGITGCGV	FKEVKADLYNS	WQNL	LYDVNGN
Consensus	(641)	ILGV	CVNYDLYGITGCGIF	VEVNATYYNS	WQNL	LYDSNGN
Section 18						
	(681)	681	690	700	710 720	
human coronavirus OC43 S	(657)	LYGERDY	ITNRTFMIRSCYSG	RVSAAFHANS	SEPA	LLERN
avianinfectiousbronchitisvirusS	(465)	ELDTSG	SIDIFVVQGEYGLN	YYKVN	PCE	DVNQFV
bovine coronavirus S	(667)	LYGERDY	ITNRTFMIRSCYSG	RVSAAFHANS	SEPA	LLERN
mouse hepatitis virus S	(616)	LYGERDL	TNKTITIRSCYSG	RVSAAFH	KDA	EPALBYRN
Consensus	(681)	LYGERDY	ITNRTFMIRSCYSG	RVSAAFHANS	SEPA	LLERN

FIGURE 4F (contd.)

Section 19						
	(721)	721	730	740	750	760
human coronavirus OC43 S	(697)	IKCNYVFENN	SLRQLQPINY	FDSYLGCVVN	AYNSTAI	SVQ
avianinfectiousbronchitisvirusS	(505)	EVGILTSRNET	GSQLENDQ	EYIKITNGTR	RFRRSIT	ENVA
bovine coronavirus S	(707)	IKCNYVFENN	TLRQLQPINY	FDSYLGCVVN	ADNSTS	SVQ
mouse hepatitis virus S	(656)	INCXYVES	INTSREEN	PENYFDSY	LGCVVN	ADNRITD
Consensus	(721)	IKCNYVFENN	SLRQLQPINY	FDSYLGCVVN	ADNSTS	EAVQ
Section 20						
	(761)	761	770	780	790	800
human coronavirus OC43 S	(737)	TCDLTVGSGY	CVDYSKNRR	SRGATITG	YRFTNNE	PFTVNS
avianinfectiousbronchitisvirusS	(545)	NEPYVSYCKE	ELTKPDG	-----	SIATIVE	EKQL
bovine coronavirus S	(747)	TCDLTVGSGY	CVDYSTKR	RSRSTITG	YRFTNNE	PFTVNS
mouse hepatitis virus S	(696)	NCDLRMGAGL	CVDYSKSR	RAIRSYST	GYRLTTE	FPPTML
Consensus	(761)	TCDLTVGSGY	CVDYSK	RRSR	SITTYR	FTNNEPFTVNS
Section 21						
	(801)	801	810	820	830	840
human coronavirus OC43 S	(777)	VNDSLEPVGG	LYEIQIPSE	FTIGNMVE	FIQTSSP	KVTIDC
avianinfectiousbronchitisvirusS	(571)	EQFVAPLFNV	TENMLLNS	SNITVTDT	YIOTRMD	QINC
bovine coronavirus S	(787)	VNDSLEPVGG	LYEIQIPSE	FTIGNME	FIQTSSP	KVTIDC
mouse hepatitis virus S	(736)	VNDSVQSV	DGLYEMO	PTNETT	IGHETE	FIQTRSP
Consensus	(801)	VNDSLEPVGG	LYEIQIPSE	FTIGNME	FIQTSSP	KVTIDC
Section 22						
	(841)	841	850	860	870	880
human coronavirus OC43 S	(817)	AAEVCGDYAA	CKSQLVEY	GSFCDN	INAILTE	VNELLD
avianinfectiousbronchitisvirusS	(611)	LQVACGSSLD	ARKLFQQ	SGPVLD	MLSVVNS	VCGKE
bovine coronavirus S	(827)	AAEVCGDYAA	CKSQLVEY	GSFCDN	INAILTE	VNELLD
mouse hepatitis virus S	(776)	AAEVCGDN	TAQSQLVE	GSFCV	VNAILTE	VNNLLNMQ
Consensus	(841)	AAEVCGDYAA	CKSQLVEY	GSFCDN	INAILTE	VNELLD
Section 23						
	(881)	881	890	900	910	920
human coronavirus OC43 S	(857)	LQVANS	LMNGVTL	STKLK	DGVN	FNVD
avianinfectiousbronchitisvirusS	(651)	NEYSSTKP	-----	AGNT	TPVLSN	VSTGE
bovine coronavirus S	(867)	LQVANS	LMNGVTL	STKLK	DGVN	FNVD
mouse hepatitis virus S	(816)	LQVASA	LMOGVT	LTSSRL	PDGTS	GP
Consensus	(881)	LQVASS	LMNGVTL	STKLK	DGVN	FNVD
Section 24						
	(921)	921	930	940	950	960
human coronavirus OC43 S	(897)	CSKASS	-----	RSAT	EDLL	FDK
avianinfectiousbronchitisvirusS	(686)	SRKRS	-----	LTE	CLL	FTS
bovine coronavirus S	(907)	CKNVSS	-----	RSAT	EDLL	FDK
mouse hepatitis virus S	(856)	CAEDGNGPS	AIRGRSA	EDLL	FDK	KLSD
Consensus	(921)	CAKSS	-----	RSAT	EDLL	FDK

FIGURE 4F (contd.)

Section 25					
	(961)	961	970	980	990 1000
human coronavirus OC43 S	(930)	GGAE	--IRDLCVQSYKGIKVTLPPL	SENQISGYTLAATS	
avianinfectiousbronchitisvirusS	(717)	ACPLGFEKDLACAREYNGLMLPPL	ITAEQALYTSSLVA		
bovine coronavirus S	(940)	GAEE	--IRDLCVQSYNGIKVLPPL	SENQISGYTLAATS	
mouse hepatitis virus S	(896)	GGQE	--VRDLICVOSENGIKVLPPL	SEQISGYTTGATA	
Consensus	(961)	GGAE	IRDLCVQSYNGIKVLPPL	SENQISGYTLAATA	
Section 26					
	(1001)	1001	1010	1020	1030 1040
human coronavirus OC43 S	(968)	ASLPPRWTAAAGVPPYLNQYRIR	INGLGVIMDVLSQNKLI		
avianinfectiousbronchitisvirusS	(757)	SMAAGGITAAAGATPEATQDAR	IMHLCITQSILLKNGEKI		
bovine coronavirus S	(978)	ASLPPWSSAAAGVPPYLNQYRIR	INGHGVIMDVLSQNKLI		
mouse hepatitis virus S	(934)	AAMPPWSAAAGVPPSHSVQYRIR	INGLGVIMNMLSENQKMT		
Consensus	(1001)	ASLPPWSAAAGVPPYLNQYRIR	INGLGVIMDVLSQNKLI		
Section 27					
	(1041)	1041	1050	1060	1070 1080
human coronavirus OC43 S	(1008)	NATNNLYATLEEDATNSALVK	DAVNANAEALNLL		
avianinfectiousbronchitisvirusS	(797)	NASNNKATGHMOEGERSLSLE	QDQDMVSKOSAITETM		
bovine coronavirus S	(1018)	ANATNNALGATQEGTDA	NSALVKDAVNANAEALNLL		
mouse hepatitis virus S	(974)	ESATNNALGATQDLEDA	NSALVGKIOSVNANAEALNLL		
Consensus	(1041)	ANAFNNALGATIQEGF	DATNSALVKIQAVVNANAEALNLL		
Section 28					
	(1081)	1081	1090	1100	1110 1120
human coronavirus OC43 S	(1048)	QQLSNRFGAISASLQEI	LSRLDALEANAQIDRLINGRLTA		
avianinfectiousbronchitisvirusS	(837)	ASENKNEGALFSVQDQAIYQ	QDFDATORNAQVDRLITGR	SS	
bovine coronavirus S	(1058)	QQLSNRFGAISASLQEI	LSRLDALEANAQIDRLINGRLTA		
mouse hepatitis virus S	(1014)	NQLSNRFGAISASLQEI	LSRLDALEANAQIDRLINGRLTA		
Consensus	(1081)	QQLSNRFGAISASLQEI	LSRLDALEANAQIDRLINGRLTA		
Section 29					
	(1121)	1121	1130	1140	1150 1160
human coronavirus OC43 S	(1088)	LNAYVSQQLSDSTLVKESAAQAME	KVNECVKSQSSRINFC		
avianinfectiousbronchitisvirusS	(877)	LSVLAASAKQAEYIRVSQORE	LATORNMECVKSQSIRYSEC		
bovine coronavirus S	(1098)	LNAYVSQQLSDSTLVKESAAQAME	KVNECVKSQSSRINFC		
mouse hepatitis virus S	(1054)	LNAYVSQQLSDSTLVKESAAQAME	KVNECVKSQSSRINFC		
Consensus	(1121)	LNAYVSQQLSDSTLVKESAAQAME	KVNECVKSQSSRINFC		
Section 30					
	(1161)	1161	1170	1180	1190 1200
human coronavirus OC43 S	(1128)	GNGNHIISLVQNAPYGLYFI	HFYSYVPTSFVTAKVSPGLCI		
avianinfectiousbronchitisvirusS	(917)	GNGRHVLTTPONANGELV	LHFSMTDSEVNVTATVEE	GV	
bovine coronavirus S	(1138)	GNGNHIISLVQNAPYGLYFI	HFYSYVPTSFVTAKVSPGLCI		
mouse hepatitis virus S	(1094)	GNGNHIISLVQNAPYGLYFI	HFYSYVPTSFVTAKVSPGLCI		
Consensus	(1161)	GNGNHIISLVQNAPYGLYFI	HFYSYVPTSFVTAKVSPGLCI		

FIGURE 4F (contd.)

Section 31					
(1201)	1201	1210	1220	1230	1240
human coronavirus OC43 S (1168)	AGDRG-----	IAPKSYFVNVNNTWMYTGSGYYPEPIT			
avianinfectiousbronchitisvirusS (957)	KPANASQYAIVPANGROIFTQVNGSMYITARDMMPRAIT				
bovine coronavirus S (1178)	AGDRG-----	IAPKSYFVNVNNTWMFTGSGYYPEPIT			
mouse hepatitis virus S (1134)	SGDRG-----	SAPKAYFMQDDGEWKEFGSSYYYPEPIT			
Consensus (1201)	AGDRG	IAPKSGYFVNVNNTWMFTGSGYYYPEPIT			
Section 32					
(1241)	1241	1250	1260	1270	1280
human coronavirus OC43 S (1202)	ENNVVVMSTCAVNYTKAPVMLNTSIP-NLPDFKEELDQW				
avianinfectiousbronchitisvirusS (997)	AGDVMTLITSQANYVSVNKTVAITTFMDNDDDFDNDLSKW				
bovine coronavirus S (1212)	ENNVVVMSTCAVNYTKAPDVMLNISTP-NLPYFKEELDQW				
mouse hepatitis virus S (1168)	DNNSVMTSSCAVNYTKAPEVFLNTSIP-NPPDFKEELDQW				
Consensus (1241)	ENNVVVMSSCAVNYTKAPDVMLNTSIP	NLPDFKEELDQW			
Section 33					
(1281)	1281	1290	1300	1310	1320
human coronavirus OC43 S (1241)	EKNQTSVAPDLSLDY--	INVTFLDLQV	EMNRIQEA	IKVLN	
avianinfectiousbronchitisvirusS (1037)	WNTDKHELEDFDKEN--	YTVPIELIDSE	EDDFKGV	TOGIN	
bovine coronavirus S (1251)	EKNQTSVAPDLSLDY--	INVTFLDLQD	EMNRIQEA	IKVLN	
mouse hepatitis virus S (1207)	EKNQTSIAPDLSLDREKLN	TL	QITY	MNRIQDA	KKLN
Consensus (1281)	EKNQTSVAPDLSLDY	INVTFLDLQ	EMNRIQEA	IKVLN	
Section 34					
(1321)	1321	1330	1340	1350	1360
human coronavirus OC43 S (1279)	QSYINLKDIGTYEYVVKWPWYVWLLIGLAGVAMLVLLFFI				
avianinfectiousbronchitisvirusS (1075)	DEILDDEKESILKTA	EWQNLVTEA	AFATTIFLL	LGWV	
bovine coronavirus S (1289)	QSYINLKDIGTYEYVVKWPWYVWLLIGLAGVAMLVLLFFI				
mouse hepatitis virus S (1247)	ESYINLKDVGTYEM	VKWPWYVWLL	GLAGVAVCVL	LLFFI	
Consensus (1321)	QSYINLKDIGTYEYVVKWPWYVWLLIGLAGVAMLVLLFFI				
Section 35					
(1361)	1361	1370	1380	1390	1400
human coronavirus OC43 S (1319)	CCCTGCG-----	TSCFKKCGGCCDDYTGHQELVIKT			
avianinfectiousbronchitisvirusS (1115)	FFMTGCGCGCCGCFGIMPLMSTUCKKSGYETTFDNDVYTE				
bovine coronavirus S (1329)	CCCTGCG-----	TSCFKKCGGCCDDYTGHQELVIKT			
mouse hepatitis virus S (1287)	CCCTGCG-----	SCCFKACGNCDDYTGGHODSLVIH			
Consensus (1361)	CCCTGCG	TSCFKKCGGCCDDYTGHQELVIKT			
Section 36					
(1401)	1401	1408			
human coronavirus OC43 S (1350)	SHDD----		SEQ ID NO:	9918	
avianinfectiousbronchitisvirusS (1155)	QYRPKKS	V	SEQ ID NO:	9909	
bovine coronavirus S (1360)	SHED----		SEQ ID NO:	9891	
mouse hepatitis virus S (1318)	NISSHED-		SEQ ID NO:	9902	
Consensus (1401)	SHDD				

FIGURE 5

Section 15					
	(589)	589	600	610	620 630
human coronavirus OC43 S	(565)	NS	ETORPQAFLLGW	ASCLQGDKCNIFANFILH	VDVNSGLTCS
bovine coronavirus S	(575)	NPCTCQ	PQAFLLGW	VDSCLOGDRCNIFANFILH	VDVNSGLTCS
mouse hepatitis virus A59 S	(524)	KGCI	CANNSTLLGW	SHITLAVNDR	COLFANILLNGLNSGLTCS
Consensus	(589)	N	CTC PQAFLLGWS	DSCLOGDRCNIFANFILH	VDVNSGLTCS
Section 16					
	(631)	631	640	650	660 672
human coronavirus OC43 S	(607)	TDLQKANTD	IILGVCVNYD	LYGITGQGIFVEVN	NATYYNSWQN
bovine coronavirus S	(617)	TDLQKSN	TDIILGVCVNYD	LYGITGQGIFVEVN	NATYYNSWQN
mouse hepatitis virus A59 S	(566)	TDLQLENT	LEVYTCLEVKYD	LYGITGQGIFVEVN	NATYYNSWQN
Consensus	(631)	TDLQKANTD	IILGVCVNYD	LYGITGQGIFVEVN	NATYYNSWQN
Section 17					
	(673)	673	680	690	700 714
human coronavirus OC43 S	(649)	LLYDSNGN	LYGFRDYITN	RTFMIRSCYSGRV	SAAFHANSSEP
bovine coronavirus S	(659)	LLYDSNGN	LYGFRDYITN	RTFMIRSCYSGRV	SAAFHANSSEP
mouse hepatitis virus A59 S	(608)	LLYDSNGN	LYGFRDYITN	RTFMIRSCYSGRV	SAAFHANSSEP
Consensus	(673)	LLYDSNGN	LYGFRDYITN	RTFMIRSCYSGRV	SAAFHANSSEP
Section 18					
	(715)	715	720	730	740 756
human coronavirus OC43 S	(691)	ALLFRNIK	CNYVFENSL	SRQLQPINYFDS	YLGCVVNADNSTA
bovine coronavirus S	(701)	ALLFRNIK	CNYVFENSL	SRQLQPINYFDS	YLGCVVNADNSTA
mouse hepatitis virus A59 S	(650)	ALLFRNIK	CNYVFENSL	SRQLQPINYFDS	YLGCVVNADNSTA
Consensus	(715)	ALLFRNIK	CNYVFENSL	SRQLQPINYFDS	YLGCVVNADNSTA
Section 19					
	(757)	757	770	780	798
human coronavirus OC43 S	(733)	ISVQTCD	LTVGSGYCV	DYSKRRSR	RSITTG
bovine coronavirus S	(743)	SVVQTCD	LTVGSGYCV	DYSKRRSR	RSITTG
mouse hepatitis virus A59 S	(692)	EALPNC	DERMAGLE	VDYKSSAA	HRSVS
Consensus	(757)	AVQTC	DLTVGSGYCV	DYSKRRSR	RSITTG
Section 20					
	(799)	799	810	820	830 840
human coronavirus OC43 S	(775)	NS	VDLSLEPVGGLYEI	QIPSEFTTIGNM	EEFIQTSSPKVTIDC
bovine coronavirus S	(785)	NS	VDLSLEPVGGLYEI	QIPSEFTTIGNM	EEFIQTSSPKVTIDC
mouse hepatitis virus A59 S	(734)	MLND	WQSVDCGIFTEM	QITNEATCHHE	FIQTSSPKVTIDC
Consensus	(799)	NSVND	SLEPVGGLYEI	QIPSEFTTIGNM	EEFIQTSSPKVTIDC
Section 21					
	(841)	841	850	860	870 882
human coronavirus OC43 S	(817)	AAFVCGD	YAACKSQLVEY	GSFCDNINAILTE	VNELLDTTQLQ
bovine coronavirus S	(827)	SAFVCGD	YAACKSQLVEY	GSFCDNINAILTE	VNELLDTTQLQ
mouse hepatitis virus A59 S	(776)	AAFVCGD	YAACKSQLVEY	GSFCDNINAILTE	VNELLDTTQLQ
Consensus	(841)	AAFVCGD	YAACKSQLVEY	GSFCDNINAILTE	VNELLDTTQLQ

FIGURE 6

FIGURE 6A

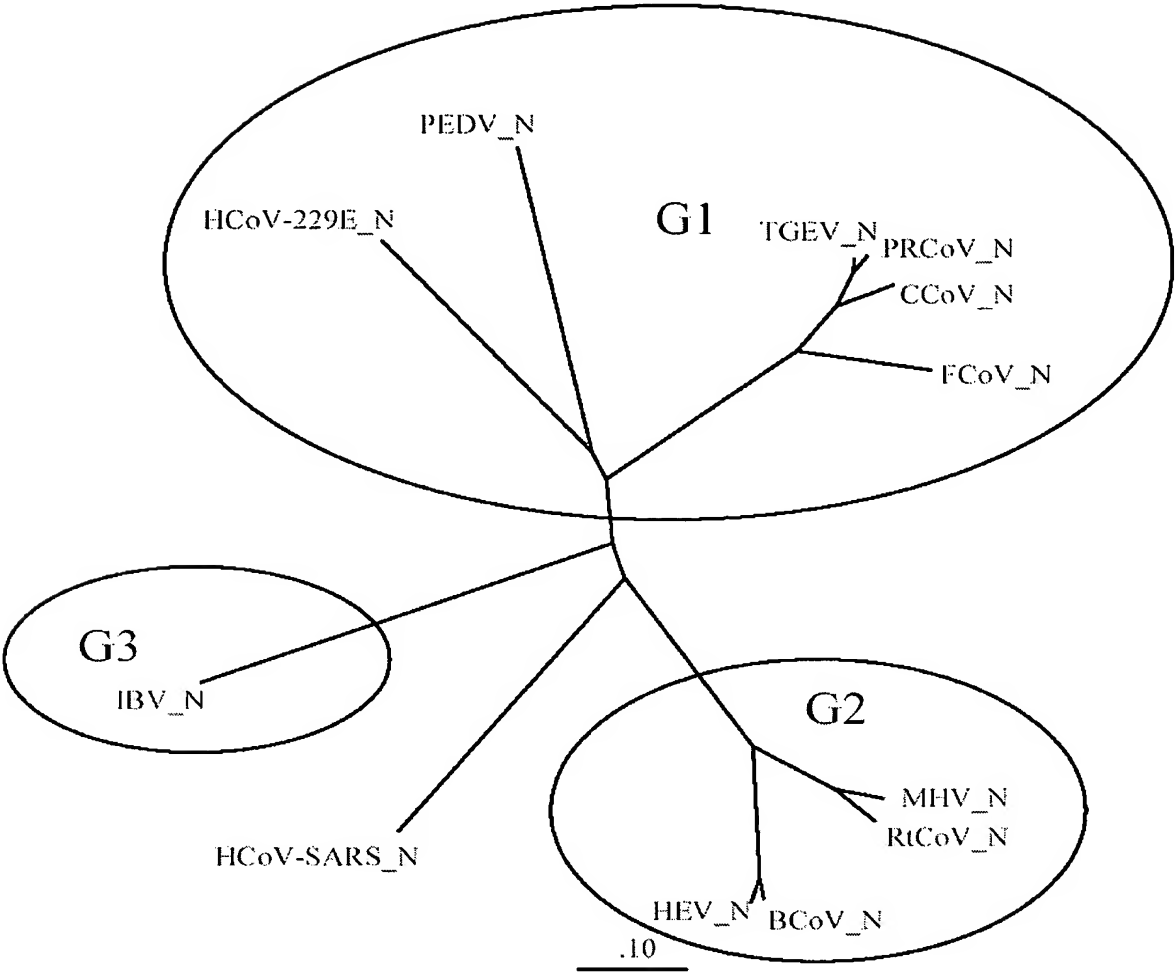


FIGURE 6B

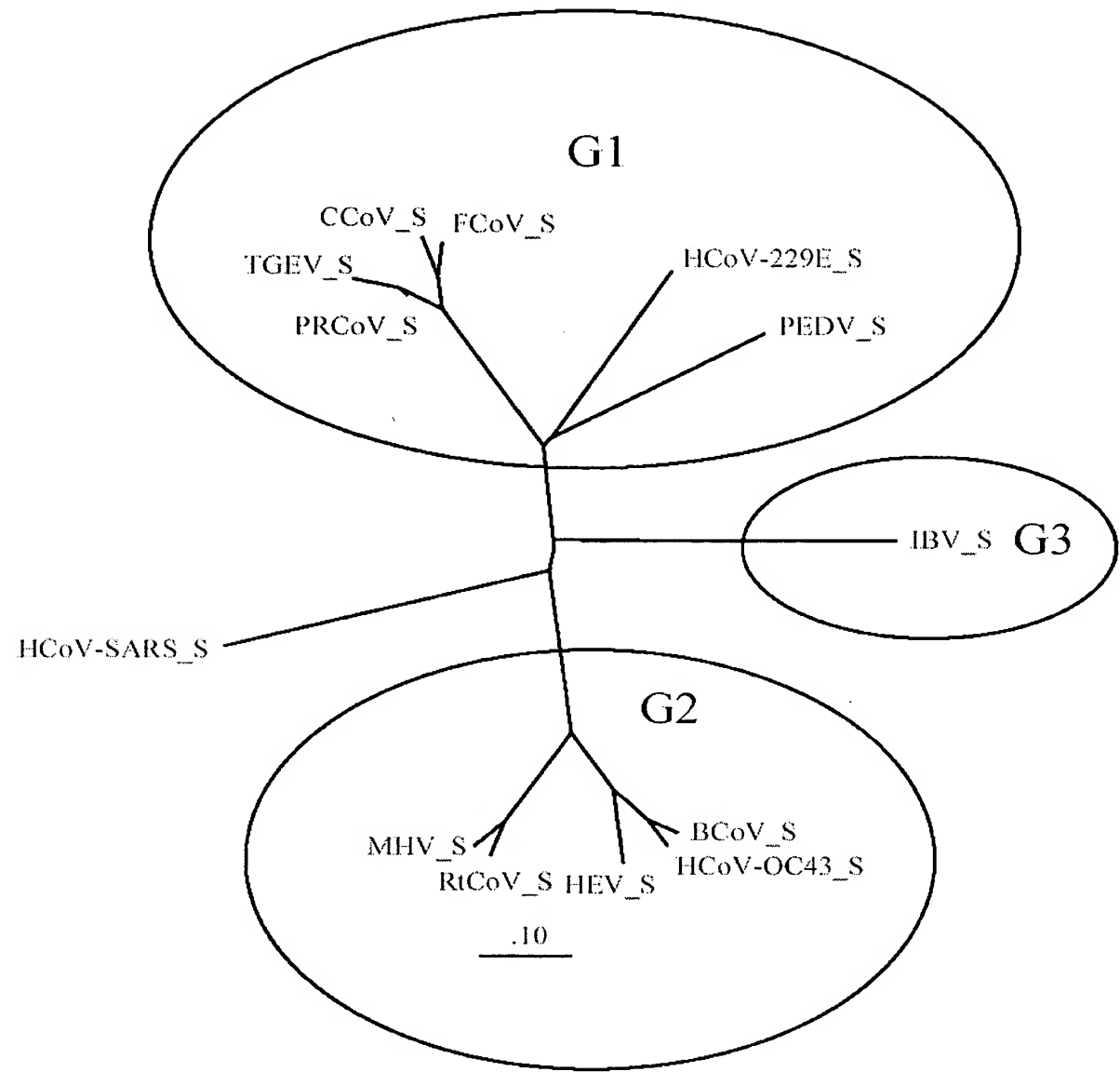


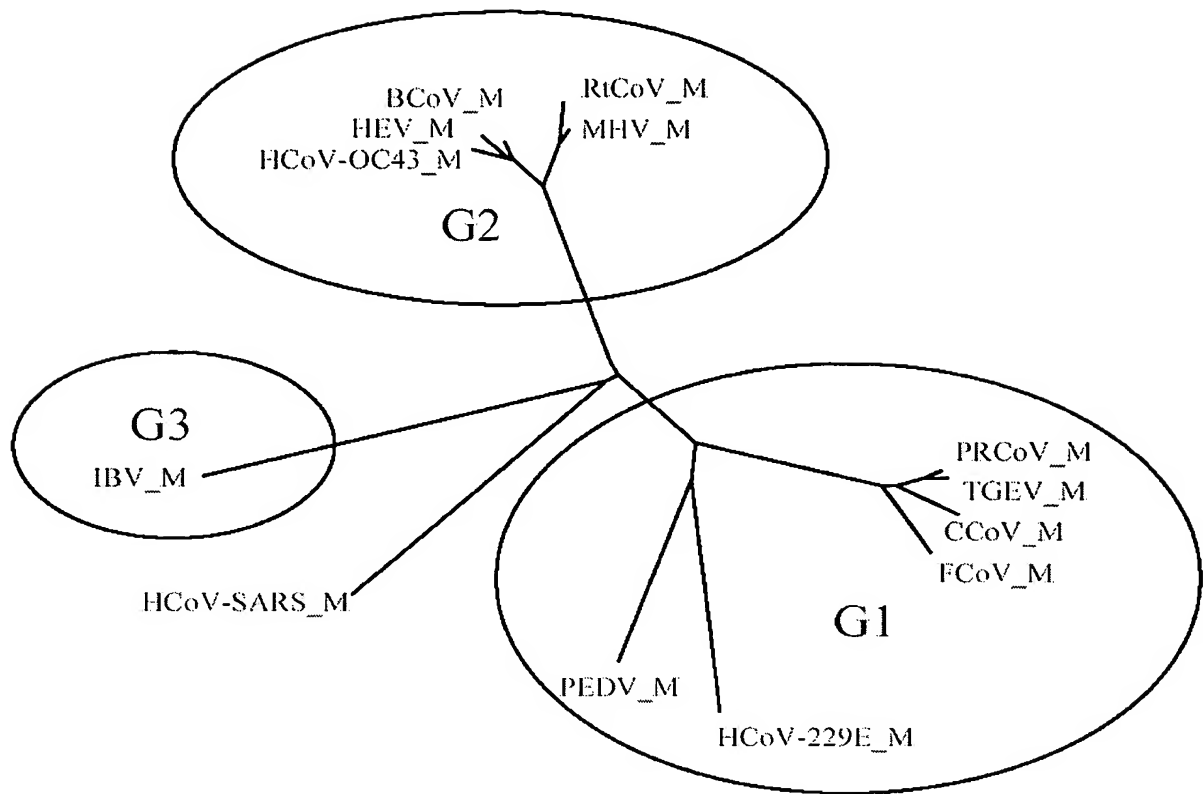
FIGURE 6C

FIGURE 7**FIGURE 7A**

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SEQ ID NO:6053 -----MFVLLVAYALLH----- 12
SEQ ID NO:6057 ---MKKLFVVLVVMPLIYGDNFPCSKLTNRTIGNQWNLIETFLNYSRLPPNSDVVLGD 60
SEQ ID NO:6061 ---MRSLIYFWLLLPVLP TSLPQDVTRCQSTTNFRFFSKFN-----VQAPAVVVLGG 52
SEQ ID NO:6065 -----MFLILLISLPTAFAVIGDLKCTTVS-INDVDTGVPSIS----- 38
SEQ ID NO:6069 -----MLFVFILFLPSCLG YIGDFRCIQLVNSNGANVSAPSIS----- 40
SEQ ID NO:6042 -----MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRG----- 39
SEQ ID NO:6072 -----MLVTPLLLVTL L CALCSAVLYDSSS----- 27
      :. : .

SEQ ID NO:6053 -----
SEQ ID NO:6057 YFPTVQPWFNCIRNDSNDLYVTLENLKALYWDYATENITWNHRQRLNVVNGYPYSITVT 120
SEQ ID NO:6061 YLPSMNSSSWYCGTG IETASGVHGI FLSYIDSGQGFEIGISQEP-----FDP SGYQLYLH 107
SEQ ID NO:6065 -----TDTVDVTNGLGTY YVLD R VYLN T TLLNG-----YY 69
SEQ ID NO:6069 -----TETVEVSQGLGTY YVLD R VYLNAT LLLTG-----YY 71
SEQ ID NO:6042 -----VYYPDEIFRSDTLYLTQDLFLPFYSNVTGFHTINHTFG-----NP 79
SEQ ID NO:6072 -----YVYYYQSAFRPPSGWHLQG----- 46

SEQ ID NO:6053 -----IAGCQTTN-----GLNTSYSVCNG----- 31
SEQ ID NO:6057 TTRNFNSAEGAI ICICKGSPPTTTTESSLTCNWGSECLNHKFPICPSNSEANCGNMLYG 180
SEQ ID NO:6061 KATNGNTNAIARLRICQFPDNKTLGPTVNDVTTGRNCLFNKAI PAYMRDGKD I VVGITWD 167
SEQ ID NO:6065 PTSGSTYRNMAL KGT LLLSTLWFKPPFLSDFTNGIFAKVKNTKVIKDGVMYSEFPAITIG 129
SEQ ID NO:6069 PVDGSKFRNLALTGTNSVSLSWFQPPYLSQFNDGIFAKVQNLKTSTPSGATAYFPTIVIG 131
SEQ ID NO:6042 VIPFKDGIYFAATEKSNNVVRGWVFGSTMNKKSQSVIIINNSTNVVIRACNFELCDNPFFA 139
SEQ ID NO:6072 -----GAYAVVNISSEFN NAGSSSGCTVGIIHGGRVVNASSIAMTAP----- 88

SEQ ID NO:6053 -----
SEQ ID NO:6057 LQWFADEVVAYLHGAS YRISFENQWSGTVTFGDMRATTL E VAGTLVDLWFWNPVYDVSYY 240
SEQ ID NO:6061 -----NDRVTVFADKIYHFY LKNDWSRVATRCYNRRSCAMQYVYTPTYMLN----- 214
SEQ ID NO:6065 -----STFVNTSYSVV VQPHTTILGNK LQGFLEISVCQYTMCEYPNT 171
SEQ ID NO:6069 -----SLFGYTSYTVVIEPYN-----GVIMASVCQYTICLLPYT 165
SEQ ID NO:6042 VS-----KPMGTQHTMI FDN A FN----- 158
SEQ ID NO:6072 -----

SEQ ID NO:6053 -----CVGYSENVFAVESGGYIPSDFAFNNWFLLTNTSSVVDGVVRSF 74
SEQ ID NO:6057 RVNNKNGTTVVSNCTDQCASYVANVFTTQPGGFIPSDFSFNNWFLLTNSSTLVSGKLVTK 300
SEQ ID NO:6061 VTSAGEDGIYYE PCTANCTGYAANVFATDSNGHIPEGFSFNNWFLLSNDSTLLHGKVVS N 274
SEQ ID NO:6065 ICNPN-LGNQRVELWHWDTG VVSCLYKRNF TYDNADYLYFHFYQEGGTFYAYFTDTGVV 230
SEQ ID NO:6069 DCKPNTNGNKLIGFWHTDVKPPICVLKRNF TLNVNADAFYFHFYQHGGTFYAYYADKPSA 225
SEQ ID NO:6042 -CTFEYISDAFSLDVSEKSGNFKHLREFVFNKDGFLYVYKGYQPIDVVRDLPSGFNTLK 217
SEQ ID NO:6072 -----SSGMAWSSSQFCTAHCNFSDTTVFVTHCYKHGG--CPLTGMLQQN 131

SEQ ID NO:6053 QPLLLNCLWSVSGLRFTTG FVYFNGTGRGDCKGFSSDVLSDVIRYNLNFEENLRG---T 131
SEQ ID NO:6057 QPLLVNCLWPVPSFEEAASTFCFEGAGFDQCNGAVLNNTVDVIRFNLNFTTNVQSGKGAT 360
SEQ ID NO:6061 QPLLVNCLLAI PKIYGLGQFFSFNHTMDGVCNGAAVDRAPEALRFNINDTSVILAEG---S 332
SEQ ID NO:6065 TKFLFN VYLGTVLSHYVVMPLTCN----SALTLEYWVTP L TSKQYLLAFNQDGVIFNAVD 286
SEQ ID NO:6069 TTFLFSVYIGDILTQYYVLPFICNPTAGSTFAPRYWVTP LVKRQYLFNFNQKVITS AVD 285
SEQ ID NO:6042 PIFKPLGINITNFRAILTAFSPAQDIWGTSA AAYFVG YLKPTTFMLKYDENG TITDAVD 277

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SEQ ID NO: 6072 LIRVSAMKNGQLFYNLTVSVAKYPTFRSFQCVNNLTSVYLNGDLVYTSNETIDVTSAGVY 191

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 SEQ ID NO: 6057 VFSLNTTGGVTLEISCYTVSDS-SFFSYGEIPFGVTDGPRYCYVHY---NGTALKYLGTL 416
 SEQ ID NO: 6061 IVLHTALG---TNLSFVCSNSSDPHLAIFAIPLGATEVPYYCFLKVDYNTSVYKFLAVL 389
 SEQ ID NO: 6065 CKSDFMSEIKCKTLSIAPSTGVYELNGYTVQPIADVYRRIPNLPDCN-IEAWLNDKSVPS 345
 SEQ ID NO: 6069 CASSYTSEIKCKTQSMPLSTGVYELSGYTVQPVGVYRRVANLPACN-IEEWLTARSVPS 344
SEQ ID NO: 6042 CSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSPGDVVR-FPNITNLCPFGEVFNATKFPS 336
 SEQ ID NO: 6072 FKAGGPITYKVMREVKALAYFVNGTAQDVLICDGS PRGLLACQYNTGNFSDGFYPTNSS 251

SEQ ID NO: 6053 PKTVREFVISRTGHFYINGYRYFTLGNEAVNFNVT---TAETTDFACTVALASYADVLV 242
 SEQ ID NO: 6057 PPSVKEIAISKWGHFYINGYNFFSTFPIDCISFNLT---TGDSDFVFTIAYTSYTEALV 472
 SEQ ID NO: 6061 PPTVREIVITKYGDVYVNGFGYHLGLLDAVTINFTGHGTDDVSGFWTIASNFVDALI 449
 SEQ ID NO: 6065 PLNWERKTFSNCFNMSSLSFIQAYSFTCNNIDAA----KIYGMCFSSITIDKFAIPNG 401
 SEQ ID NO: 6069 PLNWERKTFQNCNFNLSLLRYVQAESLFCNNIDAS----KVYGRCFGSISVDKFAVPRS 400
SEQ ID NO: 6042 VYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSAT----KLNDLCFSNVYADSEFVVKGD 392
 SEQ ID NO: 6072 LVKQKFIVYRENSVNTTCTLHNFIHNETGANPNPSG--VQNIQTYQTKTAQSGYYNFNF 309

SEQ ID NO: 6053 NVSQTSIANIICYNSVINRLRCDQLSFDVPDGFYSTSP--IQSVELPVSIVSLPVYHKHT 300
 SEQ ID NO: 6057 QVENTAITKVITYCNHVNNIKSCQITANLNGFYFVSS--SEVGLVNKSVVLLPSFYTH 530
 SEQ ID NO: 6061 EVQGTSIQRILYCDPVSQKCSQVAFDLDDGFYPISSRNLLSHEQPISEFVTLPSFNDHS 509
 SEQ ID NO: 6065 RKVDLQLGNLGYLQSFNYRIDTTATSCQLYYNLPAAVNS--VSRFPSTWNRFRGFTEQS 459
 SEQ ID NO: 6069 RQVDLQLGNSGFLQTANYKIDTAATSCQLHYTLPKNNVT--INNHNPSWNRRYGFENDAG 458
SEQ ID NO: 6042 DVRQIAPGQTGVADIADYNYKLPPDFMGCVLAWNTRNIDAT-----STGNYNKYRYLRHG 446
 SEQ ID NO: 6072 SFLSSFVYKESNFMYGSYHPSCKFRLETINGLWFNSLS-----VSIAYGPLQGCKQS 363

SEQ ID NO: 6053 FIVLYVDFKPQ-SGGGKCFNCYPAGVNITLANFNET---KGPLCVDTSHTTKYVAVYAN 356
 SEQ ID NO: 6057 IVNITIGLGMKRSYGQPIASTLS--NITLPMQDHN---TDVYCIRSDQFS-VYVHSTCK 584
 SEQ ID NO: 6061 FVNITVS-----AAFGLSSANLVASDTTNGFSS-----FCVDTRQFTITLIFYNVTN 557
 SEQ ID NO: 6065 VFKPQPAGVFTDHDVVYAQHCFASTNFCPCCKLDGSLCVGNPGIDAGYKTSIGTCPCAG 519
 SEQ ID NO: 6069 VFGKN-----QHDVVYAQQCFTRSSYPCP----- 483
SEQ ID NO: 6042 KLRPFER----- 453
 SEQ ID NO: 6072 VFKGRAT----- 370

SEQ ID NO: 6053 VGRWS-----ASINTGNCPFSFGKVNNFVKFGSVCFSCLKDIPGGCAMPIVA 402
 SEQ ID NO: 6057 SALWDNIFKRNCTDVLDAVIAIKTGTCPFSFDKLNLYLTFNKFCLSLSPVGANCKFDVAA 644
 SEQ ID NO: 6061 SYGYVS-----KSQDSNCPFTLQSVNDYLSFSKFCVSTSLLAGACTIDLFG 603
 SEQ ID NO: 6065 TNYLTCHNAAQCDCCLCTPDPITSKATGPYKCPQTKYLVGIGEHCSGLAIKSDHCG---G 575
 SEQ ID NO: 6069 -----AQPDIVSPCTT---QTKPKSAFVNVDHCEGLGVLEDNCGNADPH 525
SEQ ID NO: 6042 -----DISNVFFSPDGKPCPTPPALNCYWLND 480
 SEQ ID NO: 6072 -----CCYAYSYGGPSLCKGVYSGELDHNFECEGL 399

SEQ ID NO: 6053 NWAYSKY---YTIG-----SLYVSWSDGDGITGVPQVEGVSSFMNVTLDKC 446
 SEQ ID NO: 6057 -RTRTNE---QVVR-----SLYVIYEEDNIVGVPSDNGSVHDLVSLHLDSC 687
 SEQ ID NO: 6061 YPAFGSG---VKLT-----SLYFQFTKGELITGTPKPLEGITDVSFMTLDVC 647
 SEQ ID NO: 6065 NPCTCQP---QAFLGWSVSDCLQGDRCNIFANFILHDVNSGTTCTDLQKSNTDIILGVC 632
 SEQ ID NO: 6069 KGCICAN---NSFIGWSHDTCVLNDRQCIFANILLNGINSGTTCTDLQLPNTVEVVTGIC 582
SEQ ID NO: 6042 YGFYTTTGIGY-----QPYRVVLSFELLNAPATVCGPKLSTDLIKNQ 524
 SEQ ID NO: 6072 LVYVTKS-----GGSRIQTATEPPVITQNNYNNITLNTC 433

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SEQ ID NO: 6053 TKYNIYDVSGVGIVRVSNDTFLN-----GITYTSTSGNLLGFKDVTKGTIYSITPC 497
SEQ ID NO: 6057 TDYNIYGRGTGVGIIRQTNRTLLS-----GLYYTSLSGDLLGFKNVSDGVIYSVTPC 738
SEQ ID NO: 6061 TKYTIYGFKEGEGITLTNSSLILA-----GVYYTSDSGQLLAFKNVTSAGVYSVTPC 698
SEQ ID NO: 6065 VNYDLYGITGQGI FVEVNATYYNS-----WQNLLYDSNGNLYGFRDYL TNRTFMIRSC 685
SEQ ID NO: 6069 VKYDLYGITGQGV FKEVKADYYNS-----WQTLLYDVNGNLNGFRDL TNKTYTIRSC 635
SEQ ID NO: 6042 VNFNFNGLTGTGVLTPSSKRFP-----FQQFGRDVSDFTDSDVRDPKTSEILDISP 576
SEQ ID NO: 6072 VDYNIYGRGTGQGFITNVTDSAVSYNYLADAGLAILDTSGSIDIFVQGEYGLNYYKVNPC 493
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SEQ ID NO: 6053 NPPDQLVVYQQA--VVGAMLSENFSTSYGFSNVVELPKFFYASNGTYN----- 542
SEQ ID NO: 6057 DVSAQAVIDGT--IVGAITSINSELLGLTHWTTT PNFYYYSIYNYTNDRTGT AIDSDND 796
SEQ ID NO: 6061 SFSEQAAYVND--IVGVISSLNS--TFNNTRELPGFFYHSNDGSN----- 741
SEQ ID NO: 6065 YSGRVSAAFHAN--SSEPALLFRNIKCN YVFNNTLSRQLQPINYFDSYLGCVVNADNSTS 743
SEQ ID NO: 6069 YSGRVSAAFHKD--APEPALLYRNINCSYVFSNNISREENPLNYFDSYLGCVVNADNRD 693
SEQ ID NO: 6042 AFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFTQAGCL 636
SEQ ID NO: 6072 EDVNQQFVVSGGK-LVGILTSRNETGSQLENQFYIKITNGTRRFRRSITEN----- 544

SEQ ID NO: 6053 -CTDAVLTYSSFGVCADGS-----IIAVQPRNVSYDSVSAIVTAN-----LSI 584
SEQ ID NO: 6057 VDCEPVITYSNIGVCKNGA-----FVFINVTHSDGD-VQPISTGN-----VTI 838
SEQ ID NO: 6061 -CTEPVLVYSNIGVCKSGS-----IGYVPSQYGQVK-IAPTVTGN-----ISI 782
SEQ ID NO: 6065 SVVQTCDLTVGSGYCDYSTKRRSRRSIT TGYRFTNFEPFTVNSVND SLEPVGGLYEIQI 803
SEQ ID NO: 6069 EALPNCDLRMGAGLCVDYSKSRADR SVSTGYRLTTFEYP TMLVND SVQSV DGLYEMQI 753
SEQ ID NO: 6042 IGAHVDTSYECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNITAI 696
SEQ ID NO: 6072 VANCOPYVSYGKFCIKPDGS-----IATIVPKLEQFVAPLFNV TEN-----VLI 588
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SEQ ID NO: 6053 PSNWTTSVQVEYLQITSTPIVDCSTYVCNGNVRCVELLKQYTSACKTIEDALRNSARLE 644
SEQ ID NO: 6057 PTNFTISVQVEYIQYVTT PVSIDCSRYVCNGNPRCNKLLTQYVSACQTIEQALAMGARLE 898
SEQ ID NO: 6061 PTNFSMSIRTEYLQLYNTPVSDCATYVCNGNSRCKQLLTQYTAACKTIESALQLSARLE 842
SEQ ID NO: 6065 PSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQLVEYGSFCDNINAILTEVNELL 863
SEQ ID NO: 6069 PTNFTIGHHEEFIQTRSPKVTIDCAAFVCGDNTACRQQLVEYGSFCVNVNAILNEVNLL 813
SEQ ID NO: 6042 PTNFSISITTEVMPVSMARKTSVDCNM YICGDSTECANLLLO YGSFCTQLNRALSGIAAEQ 756
SEQ ID NO: 6072 PNSFNLTVTDEYIQTRMDKVQINCLQYVCGSSLDCKRLFQQYGPVCDNILSVNSVVGQKE 648
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SEQ ID NO: 6053 SADVSEMLTFDKKAFTLANVSSFGDYN-----LSSVIPSLPTSGS---- 684
SEQ ID NO: 6057 NMEVDSMLFVSENAKLASVEAFNSSETLDPIYKEWPNIGGSWLEGLKYILPSHNS---- 954
SEQ ID NO: 6061 SVEVNSMLTISEEALQLATISSFNGDG-----YNFTNVLGASVYDPASGR---- 887
SEQ ID NO: 6065 DTTQLQVANSMLMNGVTLSTKLKDG VNFN-----VDDINFSPVLGCLGSDCN---- 909
SEQ ID NO: 6069 DNMQLQVASALMQGVTISSRLPDGISGP-----IDDINFSPLLGCIGSTCAEDGN 863
SEQ ID NO: 6042 DRNTREVFAQVKQMYKTPTLKYFGGFN-----FSQILPDPLKPTK---- 796
SEQ ID NO: 6072 DMELLNFYSSTKPAGFNTPVLSNVSTG-----EFNISLLLTNPSSRRK---- 691
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SEQ ID NO: 6053 ---RVAGRSAIEDILFSKLVTSGLGTVDADYKKCTKGLS--IADLACAQYYNGIMVLPGV 739
SEQ ID NO: 6057 ---KRKYRSAIEDLLFDKVVTSGLGTVDEDYKRCTGGYD--IADLVCAQYYNGIMVLPGV 1009
SEQ ID NO: 6061 ---VVQKRSVIEDLLFNKVVTNGLGTVDEDYKRC SNGRS--VADLVCAQYYSGVMVLPGV 942
SEQ ID NO: 6065 ---KVSSRSAIEDLLFSKVKLS DVG-FVEAYNNCTGGAE--IRDLCVQSYNGIKVLPPL 963
SEQ ID NO: 6069 GPSAIRGRSAIEDLLFDKVKLS DVG-FVEAYNNCTGGQE--VRDLLCVQSFNGIKVLPVP 920
SEQ ID NO: 6042 -----RSFIEDLLENKVTLADAG-FMKQYGECLGDIN--ARDLICAQKFNGLTVLPPL 846
SEQ ID NO: 6072 -----RSLIEDLLFTSVESVGLP-TNDAYKNCTAGPLGFFKDLACAREYNGLLVLPPI 743
** *** : * . * . * * . : : * : * :

```


SEQ ID NO: 6053 ADAERMAMYTGSLIGGIALGGLTS----AVSIPFSLAIQARLNYVALQTDVLQENQKILA 795
 SEQ ID NO: 6057 ANADKMTMYTASLAGGITLALGGG---AVAIPFAVAVQARLNYVALQTDVLNKNQKILA 1066
 SEQ ID NO: 6061 VDAEKLHMYASLIGGMALGGITA----AALPFSYAVQARLNYLALQTDVLQRNQQLLA 998
 SEQ ID NO: 6065 LSENQISGYTLAATSASLFPPWSA----AAGVPFYLNVQYRINGIGVTMDVLSQNKLIA 1019
 SEQ ID NO: 6069 LSESQISGYTTGATAAAMFPPWSA----AAGVPFSLSVQYRINGLVTMNVLSQNKIA 976
SEQ ID NO: 6042 LTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIA 906
 SEQ ID NO: 6072 ITAEMQALYTSSLVASMAFGGITA----AGAIPFATQLQARINHLGITQSLLLNQEKIA 799
 . *: . . . * : ** : * : * : . : * . * : *

SEQ ID NO: 6053 ASFNKAMTNIVDAFTGVNDAITQTSQALQTVATALNKIQDVVNQQGNSLNHLTSQLRQNF 855
 SEQ ID NO: 6057 SAFNQAIGNITQSFQVNDIAHQTSRGLATVAKALAKVQDVVNIQQQALSHLTVQLQNNF 1126
 SEQ ID NO: 6061 ESFNSAIGNITSFAESVKEAISQTSKGLNTVAHALTKVQEVVNSQGSALNQLTVQLQHNF 1058
 SEQ ID NO: 6065 NAFNNALGAIQEGFDATN-----SALVKIQAVVNANAEALNNLLQQLSNRF 1065
 SEQ ID NO: 6069 SAFNNALGAIQDGFATN-----SALGKIQSVVNANAEALNNLLNQLSNRF 1022
SEQ ID NO: 6042 NQFNKAISQIQESLTTTS-----TALGKLQDVVNQNAQALNTLVKQLSSNF 952
 SEQ ID NO: 6072 ASFNKAIGHMQEGFRSTS-----LALQQIQDVVSKQSAILTETMASLNKNF 845
 **.*: : . : . . ** : * * . : . * . * . *

SEQ ID NO: 6053 QAISSSIQAIYDRLDTIQADQQVDRLITGRLAALNVFVSHTLTKEYTEVRASRLAQQKVN 915
 SEQ ID NO: 6057 QAISSSIDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVRASRLAKDKVN 1186
 SEQ ID NO: 6061 QAISSSIDDIYSRLDILSADVQVDRLITGRLSALNAFVAQTLTKYTEVQASRLAQQKVN 1118
 SEQ ID NO: 6065 GAISSSLQEILSRDALEAQAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAQAAMEKVN 1125
 SEQ ID NO: 6069 GAISASLQEILTRLEAVEAKAQIDRLINGRLTALNAYISKQLSDSTLIKVSAAQAIKVN 1082
SEQ ID NO: 6042 GAISSVLNDILSRDKVEAEVQIDRLITGRQLSLQTYVTQQLIRAAEIRASANLAATKMS 1012
 SEQ ID NO: 6072 GAISSVIQEIYQQFDAIQANAQVDRLITGRLSLVLASAKQAEYIRVSQQRELATQKIN 905
 ***: . : * : : . : * . * : * : * : * : * : : : : : * * :

SEQ ID NO: 6053 ECVKSQSKRYGFCG-NGTHIFSIVNAAPEGLVFLHTVLLPTQYKDVEAWSGLCDVG---- 970
 SEQ ID NO: 6057 ECVRSQSRFGFCG-NGTHLFLSLANAAPNGMIFHTVLLPTAYETVTAWPGICASDG-DR 1244
 SEQ ID NO: 6061 ECVKSQSQRYGFCGGDGEHIFSLVQAAPQGLLFLHTVLPVPGDFVNVLAIAGLCVNG---- 1174
 SEQ ID NO: 6065 ECVKSQSSRINFCEG-NGNHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAG---- 1180
 SEQ ID NO: 6069 ECVKSQTRINFCEG-NGNHILSLVQNAPYGLYFIHFSYVPISFTTANVSPGLCISG---- 1137
SEQ ID NO: 6042 ECVLGGQSKRVDFCG-KGYHLSMFPQAAPHGVFLHVTYVPSQERNFTTAPAICHEG---- 1067
 SEQ ID NO: 6072 ECVKSQSIRYSFCG-NGRHVLTIPQNAAPNGIVFIHFSYTPDSFVNVTAVGFCVKPANAS 964
 *** . * : * . * : * * : : : : * * : * : * . : *

SEQ ID NO: 6053 TNGYVLRQPNLALYK-----EGNYYRITSRIMFEPRIPTMADFVQIENCNVTFVNISRS 1024
 SEQ ID NO: 6057 TFGLVVKDVQLTLFRN-----LDDKFYLTPTMTYQPRVATSSDFVQIEGCDVLFVNATVS 1299
 SEQ ID NO: 6061 EIALTLREPGLVLFTHLQTYTATEYFVSSRRMFEPKPTVSDFVQIESCVVTVYNLTSD 1234
 SEQ ID NO: 6065 DRGIAPKSGYFVNVNN-----TWMFTGSGYYPPEPITGNNVVMSTCAVNYTKAPDV 1232
 SEQ ID NO: 6069 DRGLAPKAGYFVQDDG-----EWKFTGSSYYPPEPITDKNSVIMSSCAVNYTKAPEV 1189
SEQ ID NO: 6042 -KAYFPREGVVFVNGT-----SWFITQRNFFSPQIITDNTFVSGNCDVVGIIINNT 1118
 SEQ ID NO: 6072 QYAIVPANGRGIFIQVN-----GSYYITARDMYMPRAITAGDVVTLTSCQANYVSVNKT 1018
 . : : : * . * : . * .

SEQ ID NO: 6053 ELQTIVP-EYIDVNKTLQELSYKL-PNYTVPDLVVEQYNQTLNLTSISTLENKSAELN 1082
 SEQ ID NO: 6057 DLPSIIP-DYIDINQTVQDILENFRPNWTVPELTFDIFNATYLNLTGEIDDLERSEKLH 1358
 SEQ ID NO: 6061 QLPDVIP-DYIDVNKTLDEILASL-PNRTGPSPLPLDVFNATYLNLTGEIADLEQRSLSR 1292
 SEQ ID NO: 6065 MLNISTP-NLPYFKEELDQWFKNQTSPVAPDLSLDY--INVTFLDLQDEM----- 1279
 SEQ ID NO: 6069 FLNTSIP-NPPDFKEELDKWFKNQTSIAPDLSLDFEKLNVTLTLDLYEMN----- 1238
SEQ ID NO: 6042 VYDPLQP-ELDSFKEELDKYFKNHTSPVDLGDIG-INASVVNIQKEID----- 1166
 SEQ ID NO: 6072 VITTFVDNDDDFDNELSKWVNDTKHELPDFDKFN--YTVPILDIDSEID----- 1066
 : . : . : . . . : : * :

65/199

```

SEQ ID NO:6053 YTVQKLQTLIDNINSTLVDLKWLNRVETIYKWPWWVWLCISVVLIFVVSMLLLCCCSTGC 1142
SEQ ID NO:6057 NTTVELAILIDNINNTLVNLEWLNRIETIYKWPWYVWLLIGLVVIFCIPLLLFCCCSTGC 1418
SEQ ID NO:6061 NTTEELRSLINNINNTLVLDLEWLNRVETIYKWPWWVWLIIVIVLIFVVSLLVFCCISTGC 1352
SEQ ID NO:6065 ----RLQEAIKVLNQSYINLKDIGTYEYVYKWPWYVWLLIGFAGVAMLVLLFFICCCTGC 1335
SEQ ID NO:6069 ----RIQDAIKKLNESYINLKEVGTYEMYVYKWPWYVWLLIGLAGVAVCVLLFFICCCTGC 1294
SEQ ID NO:6042 ----RLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMTTILCCMTSC 1222
SEQ ID NO:6072 ----RIQGVIQGLNDSLIDLEKLSILKTYIKWPWYVWLAIAFATIIIFILILGWVFFMTGC 1122
      .:      . :*. : :*: :. : *:*:*:*:* : : : : *.*

SEQ ID NO:6053 CGFFSCFA-----SSIRGCCSTKLPYYD-VEKIHQ--- 1173
SEQ ID NO:6057 CGCIGCLG-----SCCHSICSRQFENYEPIEKVHVH--- 1450
SEQ ID NO:6061 CGCCGCCG-----ACFSGCCRGPRLPYEAFAFEKVHVQ--- 1384
SEQ ID NO:6065 G--TSCFK-----KCGGCCDDYTGHQELVIKT---SHED- 1364
SEQ ID NO:6069 G--SCCFK-----KCGNCCDEYGGHQDSIVIHNISSHED- 1326
SEQ ID NO:6042 CSCLKGAC-----SCG-SCCKFDEDDSEPVLGKGVKLHYT- 1255
SEQ ID NO:6072 CGCCCGCFGIMPLMSKCGKKSSYYTTFDNDVVTEQYRPKKSV 1164

```

FIGURE 7B

```

SEQ ID NO:6054 -----MFLKLVDDHA-LVVNVLLWCVVLIVILLVCITIIKLIKLCFTCHMFCNRTVY 51
SEQ ID NO:6062 -----MLQLVNDNG-LVVNVILWLFLVLFLLIISITFVQLVNLCTCHRLCNSAVY 54
SEQ ID NO:6058 ----MTFPRALTVIDDNG-MVINIIFWFLIIILILLSIALLNIIKLCMVCCNLGRTVII 59
SEQ ID NO:6045 -----MYSFVSEETGTLIVNSVLLFLAFVVFLLVTLAILTALRLCAYCCNIVNVSLV 52
SEQ ID NO:6073 -----MNLLNKSLEENG-SFLTALYIIIVGFLALYLLGRALQAFVQAADACCLEFWYTWV 57
SEQ ID NO:6066 -----MFMADAYFADTVWYVVGQIIFIVAICLLVIIVVVAFLATFKLCIQLCGMCNTLVL 54
      :      .      :      . . : : : : : :

SEQ ID NO:6054 GP----IKNVYH-IY-QSYMH-----IDPF-----PKRVIDF----- 77
SEQ ID NO:6062 TP----IGRLYR-VY-KSYMR-----IDPL-----PSTVIDV----- 80
SEQ ID NO:6058 VP----AQHAYD-AY-KNFM-----IKAYN-----PDGALLA----- 86
SEQ ID NO:6045 KP----TVYVYS-RV-KNLNS-----SEGV-----PDLLV----- 76
SEQ ID NO:6073 IPGAKGTAFVYKYTYGRKLNNPELEAVIVNEFPKNGWNNKNPANFQDAQRDKLYS 112
SEQ ID NO:6066 SP----SIYVFN-RG-RQFYEF-----YNDVKP-----PVLVDVDDV----- 84
      *      :      :.      .      *

```

FIGURE 7C

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SEQ ID NO:6055 -----MSNDNC-----TGDIVTHLKNWNF 19
SEQ ID NO:6063 -----MSNGSIP-----VDEVIEHLRNWNF 24
SEQ ID NO:6059 ----MKILLILACVIACACGERYCAMKSDTDLSCRNSTASDCESCFFNGGDLIWHLANWNF 60
SEQ ID NO:6067 -----MSSVT-TPAPVYTWT-----ADEAIKFLKEWNF 27
SEQ ID NO:6070 -----MSSTTQAPEPVYQWT-----ADEAVQFLKEWNF 33
SEQ ID NO:6046 -----MADNGTIT-----VEELKQILLEQWNL 21
SEQ ID NO:6074 -----MPNETNCTLD-----FEQSVQLFKEYNL 28
      *      .      :      : :*:

SEQ ID NO:6055 GWNVILTFIVILQFGHYKYSRLFYGLKMLVLWLLWPLVLALSIFDTWANWDSN-WAFVA 78
SEQ ID NO:6063 TWNIILTILLVVLQYGHYKYSVFLYGVKMAILWILWPLVLALSIFDAWASFQVN-WVFFA 83
SEQ ID NO:6059 SWSIILIVFITVLQYGRPQFSWFYGIKMLIMWLLWPVVLALTIFNAYSEYQVSRYVMFG 120
SEQ ID NO:6067 SLGIILLFITVILQFGYTSRSMFVYVIKMWILWLMWPLTIILTIFN--CVYALN-NVYLG 84
SEQ ID NO:6070 SLGIILLFITIILQFGYTSRSMFIYVVKMILWLMWPLTIVLCIFN--CVYALN-NVYLG 90
SEQ ID NO:6046 VIGFLFLAWIMLLQFAYSNNRNFYIIKLVFLWLLWPVTLACFVLA--AVYRIN-WVTGG 78

```

SEQ ID NO: 6074 FITAFLLFLTIILQYGYATRSKVIYTLKMIVLWCFWPLNIAVGVIS--CTYPPN-TGGLV 85
 :: : ** : . . . * : * : * : : : : .

SEQ ID NO: 6055 FSFFMAVSTLVMWVMYFANSFRLFRRARTFWAWNPEVNAITVTTVL-QQTYYPQIQQAAPT 137
 SEQ ID NO: 6063 FSILMACITLMLWIMYFVNSIRLWRRTHSWWSFNPETDALLTTSVM-GRQVCIPVLGAPT 142
 SEQ ID NO: 6059 FSIAGAIVTFVLWIMYFVRSIQLYRRTKSWSFNPETKAILCVSAL-GRSYVLPLEGVPT 179
 SEQ ID NO: 6067 FSIVFTIVAIIMWIVYFVNSIRLFIRTGSWSFNPETNNLMCIDMK-GRMYVRPIIEDYH 143
 SEQ ID NO: 6070 FSIVFTIVSIVIWIMYFVNSIRLFIRTGSWSFNPETNNLMCIDMK-GTVYVRPIIEDYH 149
SEQ ID NO: 6046 IAIAMACIVGLMWLSYFVASFRLFARTSRMWSFNPETNILLNVPLR-GTIVTRPLMESEL 137
 SEQ ID NO: 6074 AAILTVFACLSFVGWYIQSIRLEKRCRSWSFNPESNAVGSILLTNGQQCNFAIESVPM 145
 : : : : * : * : * : * : * : * : *

SEQ ID NO: 6055 GITVTLLSGVLYVDGHRLASGVQVHNLPEYMTVAVPSTTIYSRVGRSVNSQNSTG--WV 195
 SEQ ID NO: 6063 GVTLTLLSGTLLVEGYKVATGVQVSQLPNFVTVAKATTIVYGRVGRSVNASSGTG--WA 200
 SEQ ID NO: 6059 GVTLTLLSGNLYAEGFKIAGGMNIDNLPKYVMVALPSRTIVYTLVGKKLKASSATG--WA 237
 SEQ ID NO: 6067 TLTVTIIRGHLYMQGIKLTGYSLSDLPAYVTVAKVSHLLTYKRG-FLDKIGDTSG--FA 200
 SEQ ID NO: 6070 TLTATIIRGHLYMQGVKLGTGFSLSDLPAYVTVAKVSHLCTYKRA-FLDKVDGVSG--FA 206
SEQ ID NO: 6046 VIGAVIIRGHLRMAGHSLGR-CDIKDLPEKITVATS-RTLSYYKLGASQVRGTDG--FA 193
 SEQ ID NO: 6074 VLSPIIKNGVLYCEGQWLAK-CEPDHLPKDFVCTPDRRIYRMVQKYTGQSGNKKRFA 204
 : : * * * : . . ** : * . * . :

SEQ ID NO: 6055 FYVRVKHGDFAVSSPMSNMTENERLLHFF 225
 SEQ ID NO: 6063 FYVRSKHGDYSAVSNPSAVLTDSEKVLHLV 230
 SEQ ID NO: 6059 YYVKSAGDYSTEAR-TDNLSEKELLMHV 266
 SEQ ID NO: 6067 VYVKSQVGNRYRLPSTQKSGLDLALLRNNI 230
 SEQ ID NO: 6070 VYVKSQVGNRYRLPSN-KPSGADTALLR--I 233
SEQ ID NO: 6046 AYNRYRIGNYKLNTDHAGSNDNIALLVQ-- 221
 SEQ ID NO: 6074 TFVYAKQSVDTGELESVATGGSSLYT---- 230
 : : . . .

FIGURE 7D

SEQ ID NO: 6056 -----MATVKWADASE-----PQRGRQG----- 18
 SEQ ID NO: 6064 -----MASVSF-----QDRGRK----- 17
 SEQ ID NO: 6060 -----MANQQRVSWGDEST-----KTRGRSNSRGRKN----- 31
 SEQ ID NO: 6068 MSFTPGKQSSS-RASSGNRSGNGILK---WADQSDQSRNVQTRGRR-AQPKQTATSQQPS 55
 SEQ ID NO: 6071 MSFVPGQENAGGRSSSVNRAGNGLKTTWADQTERGPNNQNRGRR-NQPKQTATTQ-PN 58
SEQ ID NO: 6051 -----MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQGLPN 48
 SEQ ID NO: 6075 -----MASGKAAGKTDA PAPVIKLGPKP-----PKVGSS----- 35
 . . . *

SEQ ID NO: 6056 ----RIPYSLYSPLLVDSEQPW-KVIPRNLVPINKK-DKNKLIGYWN--VQKRFRTRKGK 70
 SEQ ID NO: 6064 ----RVPLSLYAPLRVTNDKPLSKVLANNVPTNKG-NKDQQIGYWN--EQIRWRMRGE 70
 SEQ ID NO: 6060 ---NNIPLSFFNPITLQQGSKFWNLCPDFVPKGIG-NRDQQIGYWN--RQTRYRMVKGQ 85
 SEQ ID NO: 6068 GGNVVPYYSWFSGITQFQKGKEFEFAEGQGVPIAPGVPATEAKGYWYRHNRRSEKTDAGN 115
 SEQ ID NO: 6071 SGSVVPYYSWFSGITQFQKGKEFQFAEGQGVPIANGIPASEQKGYWYRHNRRSEKTPDGQ 118
SEQ ID NO: 6051 NT-----ASWFTALTQHGK-EELRFPRGQGVPIINTNSGPDDQIGYYRRATR-VRGGDGK 101
 SEQ ID NO: 6075 ----GNASWFQAIKAKKLNTPPPKFEGSGVPDENIKPSQQHGYWR--RQARFKPGKGG 88
 * : : . ** . ** : : *

SEQ ID NO: 6056 RVDLSPKLHFYYLGTGPHKDAKFRERVEGVVWVAVDGAKEPTGYGVRRKNSEPEIPHFN 130
 SEQ ID NO: 6064 RIEQPSNWHFYYLGTGPHGDLRYRTRTEGVFWAKEGAKEPTNLGVRKASEKPIIPKFS 130
 SEQ ID NO: 6060 RKELPERWFFYYLGTGPHADAKFKDKLDGVVWVAKDGAMNKPTTLGSRGANNESKALKFD 145

SEQ ID NO: 6068 QRQLLPWYFYLLGTGPHAKDQYGTIDIGVYVWASNQADVNTPADILDRDPSSD--EAIP 173
 SEQ ID NO: 6071 QKQLLPWYFYLLGTGPHAGASYGDSIEGVFWVANSQADTNTRSDIVERDPSSH--EAIP 176
SEQ ID NO: 6051 MKELSPRWYFYLLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNN--AATV 159
 SEQ ID NO: 6075 RKPVPDAWYFYTTGTGPAADLNWGDQDQGVVWAAKGADTKSRNQGTDRDPDKF--DQYP 146
 . *** . : : *

SEQ ID NO: 6056 QKLPNGVTVVEE---PDSRAPSRQSQR-----SQSRGRGESK----- 164
 SEQ ID NO: 6064 QQLPSVVEIVEPNTPPASRANSRSRSGNGNNSRSPSNNRGNNQSRGNSQNRGNNQGRG 190
 SEQ ID NO: 6060 GKVPGEFQLEVN---QSRDNSRSRQ-----SRSRSRNR----- 176
 SEQ ID NO: 6068 TRFPPTVLPQGYIEGS-GRSAPNSR-----STSRASSRASS----- 210
 SEQ ID NO: 6071 TRFAPGTVLPQGFYVEGS-GRSAPASR-----SGSRQSRRGP----- 212
SEQ ID NO: 6051 LQLPQGTTLPKGFYAEGSRGGSQASSR-----SSRSRGNR----- 196
 SEQ ID NO: 6075 LRFSDGGPDGNFRWDFIPLNRGRSGRS-----TAASSAAASR----- 183
 : . . . : . .

SEQ ID NO: 6056 -----PQSRNPSSDRNHN-----SQDDIMKAVAAALKSLGFDKPKQEKDKKS 205
 SEQ ID NO: 6064 ASQNRGNNNNNNKSRNQSNRNQSNDRGGVTSRDDLVAAVKDALKSLGIGENPDRHKQ- 249
 SEQ ID NO: 6060 -----SQSRGRQQFNKK-----DDSVQAVLAALKKLGVDTEKQQRS- 215
 SEQ ID NO: 6068 -----AGSRSRANSNGRT-----PTSGVTPDMADQIASLVLAKLGKDAAKP 251
 SEQ ID NO: 6071 -----NNRARSSSNQRQ-----PASTVKPDMAEEIAALVLAKLGKDAQP 252
SEQ ID NO: 6051 -----NSTPGSSRGNS-----PARMASGGGETALALLLLDRLNQLSKV 235
 SEQ ID NO: 6075 -----APSREGSRGR-----SDSGDDLIARAAKIIQDQ----- 212
 . : .

SEQ ID NO: 6056 AKTGTPKPSRNQSPASSQTSKSLARSQSSETKEQKHEMQKPRWKRPNDVTSNVTQCF 265
 SEQ ID NO: 6064 ----QKPKQEKSDNSGKNTPK---KNKSRATSKERDLKDIPWRRIPKG--ENSVAACF 300
 SEQ ID NO: 6060 ----RSKSKERSNSKTRDTPK-----NENKHTWKRTAGK--GDVTRFY 253
 SEQ ID NO: 6068 ----QVTKQTAKEIRQKILN-----KPRQKRSPNK--QCTVQOCF 286
 SEQ ID NO: 6071 ----KQVTKQSAKEVRQKILN-----KPRQKRTPNK--QCFVQOCF 287
SEQ ID NO: 6051 SGKGQQQGGQTVTKSAAEASK-----KPRQKRATK--QYNTQAF 275
 SEQ ID NO: 6075 ----QKKGSRITKAKADEMAH-----RRYCKRTIPP--NYRVDQVF 247
 : : : * * :

SEQ ID NO: 6056 GPRDLH---NFGSAGVVANGVAKAGYPQFAELVPSTAAMLFDSSHIVSKESG----- 314
 SEQ ID NO: 6064 GPRGGFK---NFGDAEFVEKGVDSGYAQIASLAPNVAALLFGGNVAVRELA----- 349
 SEQ ID NO: 6060 GARSSA---NFGDTDLVANGSSAKHYPQLAECVPSVSSILFGSYWTSKEDG----- 302
 SEQ ID NO: 6068 GKRGPNQ---NFGGSEMLKLGTSDPQFPILAEALAPTAGAFFFGSRLELAKVQNLSGNLDE 343
 SEQ ID NO: 6071 GKRGPNQ---NFGGSEMLKLGTSDPQFPILAEALAPTAGAFFFGSKLELVKKN--SGGADE 342
SEQ ID NO: 6051 GRRGPEQTQGNFGDQDLIRQGTQYKHWPQIAQFAPSASAFFGMSRIGMEVTP----- 327
 SEQ ID NO: 6075 GPRTKGK-EGNFGDDKMNEEGIKDGRVTAMNLVPSHACLFGSRVTPKLQL----- 298
 * * *** . * . . : . * . : : .

SEQ ID NO: 6056 ---NTVVLTFTRVTVPKDHP---HLGKFLEELNAFTR-----EMQ 349
 SEQ ID NO: 6064 ---DSYEITYNYKMTVPKSDP---NVELLVSQVDAFKTGNAL-LQRKKEKKNKRETTLQ 401
 SEQ ID NO: 6060 ---DQIEVTFTHKYHLPKDDP---KTGQFLQQINAYAR-----PSEVAKEQR 343
 SEQ ID NO: 6068 PQKDVYELRYNGAIRFDSTLSGFETIMKVLNENLNAYQQQD---GTMNMSPKPQRQ--R 397
 SEQ ID NO: 6071 PTKDVYELQYSGAVRFDSTLPGFETIMKVLNENLNAYQKDG---GADVSPKPKQRKRR 398
SEQ ID NO: 6051 ---SGTWLTYHGAIKLDDKDPQFKNVILLNKHIDAYKTFP---PTE----- 368
 SEQ ID NO: 6075 ---DGLHLRFEFTTVVPCDDPQFDNYVKICDQCVDGVGTRPKDDEPKPKSRSSSRPATRG 355
 . : : . . . : .

SEQ ID NO: 6056 QHPLLNPFALEFNPSQTSP-----ATAEPVRDEVSIETDIIDEVN----- 389
 SEQ ID NO: 6064 QHEEAIYDDVGAPSDVTHANLEWDTAVDGGDTAVEIINEIFDTGN----- 446
 SEQ ID NO: 6060 KRKSRSKSAERSEQDVVPDALIENYTDVFDQTQVEIIDEVTN----- 385
 SEQ ID NO: 6068 GQKNGQGENDNISVAAPKSRVQKNKIRELTAEDISLLKKMDEP-----FTEDTSEI--- 448

SEQ ID NO:6071 QAEKKDEVNVSVAKPSSVQRNVSRELTPEDRSLLAQILDDGVVPDGLEDDSNV--- 454
SEQ ID NO:6051 -PKDKKKKTDEAQPLPQRQKKQPTVTLTPAA----- 399
SEQ ID NO:6075 NSPAPRQQRPKKEKKLKKQDDEADKALTSDEERNNAQLEFYDEPKVINWGDAALGENEL 414

FIGURE 7E

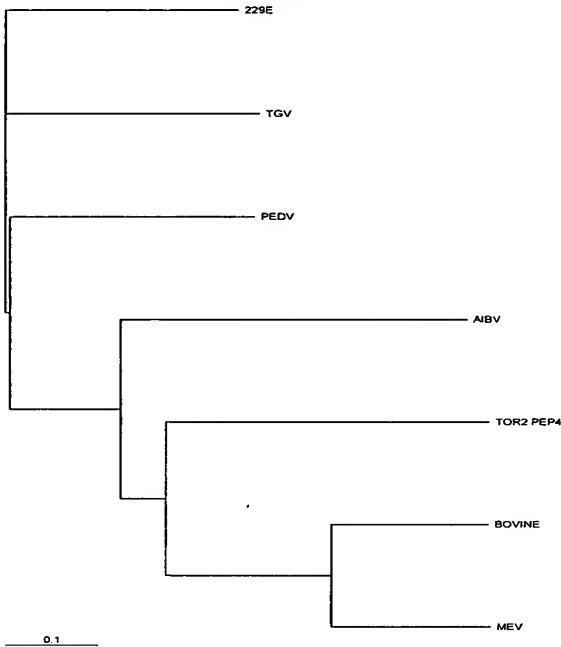


FIGURE 7F

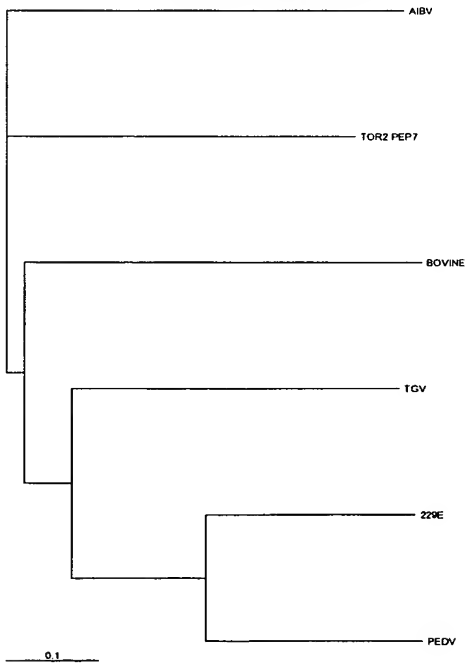


FIGURE 7G

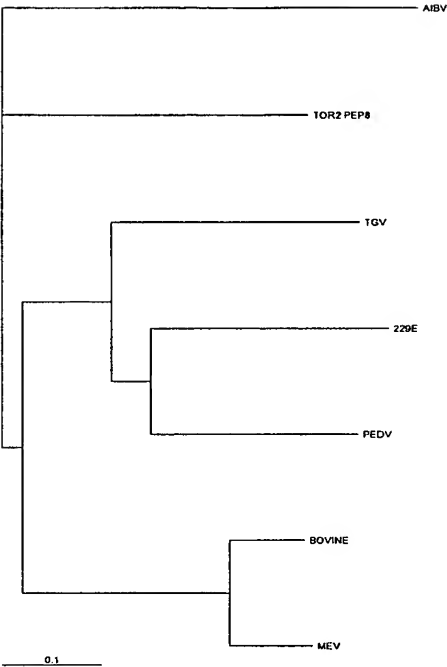


FIGURE 7H

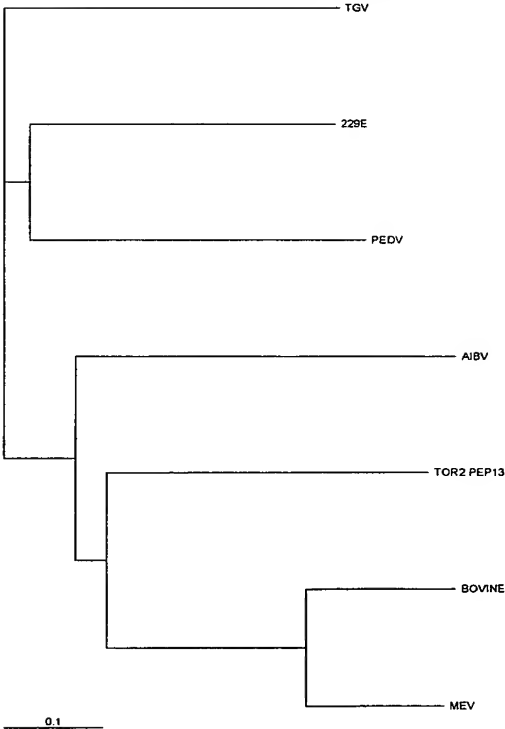


FIGURE 8

Section 1				
	(1)	10	20	30
avian IBV partial 5'UTR 161-	(1)	TATTA	AAATCTT	TATTGTTGCTGGTATCACTGCTTGT
HCoV-OC43 5'UTR	(1)	-----	-----	-----
bovine CV 5'UTR	(1)	-----	-----	-----
Consensus	(1)	-----	-----	-----
Section 2				
	(43)	43	50	60
avian IBV partial 5'UTR 161-	(43)	GTGTCTCAC	TTTATACATCTGTTGCTTGGGCTACCTAGTGTC	
HCoV-OC43 5'UTR	(1)	-----	-----	-----
bovine CV 5'UTR	(1)	-----	-----	-----
Consensus	(43)	-----	-----	-----
Section 3				
	(85)	85	90	100
avian IBV partial 5'UTR 161-	(85)	CAGCGTCCTACGGGCGTCGTGGCTGGTTCGAGTGCGAGGAAC		
HCoV-OC43 5'UTR	(1)	-----	-----	-----
bovine CV 5'UTR	(1)	-----	-----	-----
Consensus	(85)	-----	-----	-----
Section 4				
	(127)	127	140	150
avian IBV partial 5'UTR 161-	(127)	CTCTGGTTCATCTAGCCGGTAGGCGGGTGTGTGGAGTAGCA		
HCoV-OC43 5'UTR	(1)	-----	-----	-----
bovine CV 5'UTR	(1)	-----	-----	-----
Consensus	(127)	-----	-----	-----
Section 5				
	(169)	169	180	190
avian IBV partial 5'UTR 161-	(169)	TTCAGACGTACCGGTTCTGTGTGTGAAATA--CGGGGTQAC		
HCoV-OC43 5'UTR	(33)	TTCA-----	CTGATCTCTTGTAGATCTTTTGTAAATCTA	
bovine CV 5'UTR	(33)	TTCA-----	CTGATCTCTTGTAGATCTTTTTCATAATCTA	
Consensus	(169)	TTCA-----	CTGATCTCTTGTAGATCTTTTGTAAATCTA	
Section 6				
	(211)	211	220	230
avian IBV partial 5'UTR 161-	(209)	CTCCCCCACATACCTCTAAGGGCTTTTGAGCCTAGCGTTGG		
HCoV-OC43 5'UTR	(68)	AACTTTATAAAAAACATCCACTCCCTGTAGTCTATGCCTGTGG		
bovine CV 5'UTR	(68)	AACTTTATAAAAAACATCCACTCCCTGTAGTCTATGCCTGTGG		
Consensus	(211)	AACTTTATAAAAAACATCCACTCCCTGTAGTCTATGCCTGTGG		
Section 7				
	(253)	253	260	270
avian IBV partial 5'UTR 161-	(251)	GCTACGTTCTCGCATAGGTCGGCTATACGACGTTTGTAGGG		
HCoV-OC43 5'UTR	(110)	GCGTAGATTTTTCATAGTGGTGTATATATT-CATTTCT-GCT		
bovine CV 5'UTR	(110)	GCGTAGATTTTTCATAGTGGTGTCTATATT-CATTTCT-GCT		
Consensus	(253)	GCGTAGATTTTTCATAGTGGTGTCTATATT CATTTCT GCT		
Section 8				
	(295)	295	300	310
avian IBV partial 5'UTR 161-	(293)	GGTAGTGCAAAACAAGCCCTGAGGTGACAGGTTCTGGTGGTG		
HCoV-OC43 5'UTR	(150)	GTTAACAGCTTTCAGCCAGGGACGTGTTGTATCCTAGGC---		
bovine CV 5'UTR	(150)	GTTAACAGCTTTCAGCCAGGGACGTGTTGTATCCTAGGC---		
Consensus	(295)	GTTAACAGCTTTCAGCCAGGGACGTGTTGTATCCTAGGC		
Section 9				
	(337)	337	350	360
SEQ ID NO: 9910	(335)	TTTAGTGAGCAGACATACAATAGACAGTACAAACATG		
SEQ ID NO: 9919	(189)	---AGTG-GCCGCCCCATAGGTCACAATG-----		
SEQ ID NO: 9892	(189)	---AGTG-GCCACCCCATAGGTCACAATG-----		
Consensus	(337)	AGTG GCCACCCCATAGGTCACAATG		

FIGURE 9

SEQ ID NO:		
F1: AT $\frac{\text{CTT}}{\text{TGC}}$ G $\frac{\text{C}}{\text{A}}$ G $\frac{\text{GT}}{\text{CG}}$ A $\frac{\text{GGC}}{\text{TTT}}$ G $\frac{\text{G}}{\text{C}}$ GTG	(136-154 nt)	6021
F2: GTG $\frac{\text{T}}{\text{C}}$ GTG $\frac{\text{G}}{\text{C}}$ AT $\frac{\text{AG}}{\text{CC}}$ C $\frac{\text{A}}{\text{G}}$ CTTCA	(152-172 nt)	6022
F3: CTTCAC $\frac{\text{G}}{\text{T}}$ G $\frac{\text{T}}{\text{A}}$ TCT $\frac{\text{G}}{\text{C}}$ TTGT $\frac{\text{GT}}{\text{TA}}$ GA	(168-195nt)	6023
R1: AG $\frac{\text{A}}{\text{G}}$ A $\frac{\text{CCTGT}}{\text{TACAA}}$ CAC $\frac{\text{CTC}}{\text{G}}$ $\frac{\text{AGG}}{\text{CCT}}$ GG $\frac{\text{T}}{\text{C}}$ TG	(307-329nt)	6024
R2: AAA $\frac{\text{C}}{\text{T}}$ G $\frac{\text{CG}}{\text{AA}}$ TATA $\frac{\text{GC}}{\text{AA}}$ C $\frac{\text{GA}}{\text{AC}}$ C $\frac{\text{CT}}{\text{AC}}$ TATG	(265-288nt)	6025
R3: C $\frac{\text{GA}}{\text{AC}}$ C $\frac{\text{CT}}{\text{AC}}$ TATG $\frac{\text{CG}}{\text{AA}}$ A $\frac{\text{G}}{\text{A}}$ A $\frac{\text{A}}{\text{T}}$ C $\frac{\text{GTA}}{\text{TAC}}$ GCCCA	(250-274nt)	6026

FIGURE 10

					Section 1	
	(1)	1	10	20	36	
avian IBV 3'UTR (NC_001451) 27103-	(1)	GTAACATAATGGACCTGTTGTTTCCTGGTACATTTT				
HCoV-OC43 3'UTR partial	(1)	-----				
bovine CV 3'UTR	(1)	-----				
Consensus	(1)					
					Section 2	
	(37)	37	50	60	72	
avian IBV 3'UTR (NC_001451) 27103-	(37)	GTAAACACTATTTCTGTGCTTTCCATCAATTATT				
HCoV-OC43 3'UTR partial	(1)	-----				
bovine CV 3'UTR	(1)	-----				
Consensus	(37)					
					Section 3	
	(73)	73	80	90	108	
avian IBV 3'UTR (NC_001451) 27103-	(73)	ACAGGCATTGATTGTGATTATGTTCAATACTTAAGC				
HCoV-OC43 3'UTR partial	(1)	-----				
bovine CV 3'UTR	(1)	-----				
Consensus	(73)					
					Section 4	
	(109)	109	120	130	144	
avian IBV 3'UTR (NC_001451) 27103-	(109)	TTCCTTTTGGTTGCTTTTGGCTTATTGTATTGTTGCT				
HCoV-OC43 3'UTR partial	(1)	-----				
bovine CV 3'UTR	(1)	-----				
Consensus	(109)					
					Section 5	
	(145)	145	150	160	170	180
avian IBV 3'UTR (NC_001451) 27103-	(145)	GTGCTTTTTATTGTTGTGATTCTCATTAGTTTG--C				
HCoV-OC43 3'UTR partial	(1)	-----TAAGAGAAATGAAG				
bovine CV 3'UTR	(1)	-----GAGAATGAAC				
Consensus	(145)	A GAGAATGAAC				
						Section 6
	(181)	181	190	200	216	
avian IBV 3'UTR (NC_001451) 27103-	(179)	TTTATCGTAGAAATTCAATAGTAAGAGTTAAGGAAG				
HCoV-OC43 3'UTR partial	(14)	CTTAT-GTCGGCACCTGGTGGTAACCCCTC-GCAGG				
bovine CV 3'UTR	(11)	CTTAT-GTCGGCACCTGGTGGTAACCCCTC-GCAGG				
Consensus	(181)	CTTAT GTCGGCACCTGGTGGTAACCCCTC GCAGG				
						Section 7
	(217)	217	230	240	252	
avian IBV 3'UTR (NC_001451) 27103-	(215)	ATAGGCATGTAGCTTGATTACCTACATGTCTATCGC				
HCoV-OC43 3'UTR partial	(48)	AAAGTCGGG-----ATAAGGCAC-TCTCTATCAG				
bovine CV 3'UTR	(45)	AAAGTCGGG-----ATAAGGCAC-TCTCTATCAG				
Consensus	(217)	AAAGTCGGG ATAAGGCAC TCTCTATCAG				

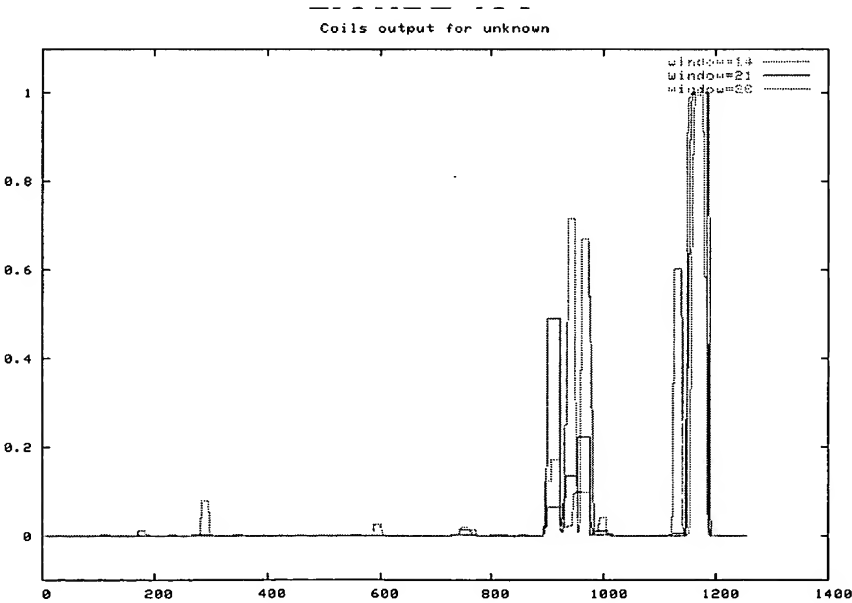
FIGURE 10 (contd.)

					Section 8	
	(253)	253	260	270	288	
avian IBV 3'UTR (NC_001451) 27103-	(251)	CAGGGA	AAATGCT	TAATCTGTCTACT	TTAGTAGCCTGG	
HCoV-OC43 3'UTR partial	(76)	AATCGA	--TGTCT	TGCTGCTATAA	TAGATAGA---G	
bovine CV 3'UTR	(73)	AATCGA	--TGTCT	TGCTGCTATAA	TAGATAGA---G	
Consensus (253)		AATGGA	TGTCT	TGCTGCTATAA	TAGATAGA G	
					Section 9	
	(289)	289	300	310	324	
avian IBV 3'UTR (NC_001451) 27103-	(287)	AAACGA	ACGCTAGAC	CCCTAGATT	TTAATTTAGTTT	
HCoV-OC43 3'UTR partial	(107)	AAGGTT	TATACCA	GAATA--	AAATAGTTG	
bovine CV 3'UTR	(104)	AAGGTT	TATACCA	GAATA--	AAATAGTTG	
Consensus (289)		AAGGTT	TATACCA	GAATA	AAATAGTTG	
					Section 10	
	(325)	325	330	340	350	360
avian IBV 3'UTR (NC_001451) 27103-	(323)	AAATTT	TTAGTTT	AGTTTAA	AGTTAGT--	TTACAGTAGG
HCoV-OC43 3'UTR partial	(139)	AAAGTT	TTTGTGT	GGTAATG	TATAGTGT	TGGAGAAAG
bovine CV 3'UTR	(136)	AAAGTT	TTTGTGT	GGTAATG	TATAGTGT	TGGAGAAAG
Consensus (325)		AAAGTT	TTTGTGT	GGTAATG	TATAGTGT	TGGAGAAAG
					Section 11	
	(361)	361	370	380	396	
avian IBV 3'UTR (NC_001451) 27103-	(358)	TATAA	AGATGCC	AGTGGCG	GGGCCAC--	GCGGAGTAC
HCoV-OC43 3'UTR partial	(175)	TG--AA	AGACT---	TGCGGA	AAGTAATT	TGCCGACAAG
bovine CV 3'UTR	(172)	TG--AA	AGACT---	TGCGGA	AAGTAATT	TGCCGACAAG
Consensus (361)		TG	AAAGACT	TGCGGA	AAGTAATT	TGCCGACAAG
					Section 12	
	(397)	397	410	420	432	
avian IBV 3'UTR (NC_001451) 27103-	(393)	GATCG	AGGGTAC	AGCACTAG	GACGCCCA	TTAGGGGA
HCoV-OC43 3'UTR partial	(206)	TGCCCA	AAGGGGA	AGAGCC	AGCAGCAC	---TTAAGTTA
bovine CV 3'UTR	(203)	TGCCCA	AAGGGGA	AGAGCC	AGCAGCATG	---TTAAGTTA
Consensus (397)		TGCCCA	AAGGGGA	AGAGCC	AGCAGCACG	TTAAGTTA
					Section 13	
	(433)	433	440	450	468	
avian IBV 3'UTR (NC_001451) 27103-	(429)	AGAGCT	AAATTT	TAGT--	TTAAGTTA	AGTTTAAAT--T
HCoV-OC43 3'UTR partial	(238)	CCACCC	AGTAATT	AGTAAAT	GAATGAAG	TTAATTAT
bovine CV 3'UTR	(235)	CCATCC	AGTAATT	AGTAAAT	GAATGAAG	TTAATTAT
Consensus (433)		CCA	CCAGTAATT	AGTAAAT	GAATGAAG	TTAATTAT
					Section 14	
	(469)	469	480	490	504	
avian IBV 3'UTR (NC_001451) 27103-	(462)	GGCTA	AGTATAG	TTAAATTT	TATAGGCT	AGTATAGA
HCoV-OC43 3'UTR partial	(274)	GGCCA	ATTGGA	AGAATCAC	-----	
bovine CV 3'UTR	(271)	GGCCA	ATTGGA	AGAATCAC	-----	
					Section 15	
	(505)	505	513			
avian IBV 3'UTR (NC_001451) 27103-	(498)	GTTAG	AGCA	SEQ ID NO: 9911		
HCoV-OC43 3'UTR partial	(293)	-----		SEQ ID NO: 9920		
bovine CV 3'UTR	(290)	-----		SEQ ID NO: 9893		
Consensus (505)						

FIGURE 11

SEQ ID NO:		
F-1	TCTATC $\frac{GCC}{AGA}$ A $\frac{G}{T}$ GGATGTCT (245 ~ 265 nt)	6027
F-2	TTAGTT $\frac{T}{G}$ AA $\frac{TT}{AG}$ TTT $\frac{A}{T}$ GT $\frac{T}{G}$ T $\frac{A}{G}$ GT (318 ~ 339 nt)	6028
F-3	TAGTGTT $\frac{A}{G}$ GAG $\frac{T}{A}$ A $\frac{G}{A}$ GT $\frac{A}{G}$ TAAAGA (346 ~ 368 nt)	6029
R-1	A $\frac{A}{C}$ TT $\frac{G}{A}$ GCCATA $\frac{A}{T}$ T $\frac{T}{A}$ AACTT (458 ~ 476 nt)	6030
R-2	ACTAA $\frac{TTAC}{AATT}$ T $\frac{G}{A}$ $\frac{C}{T}$ $\frac{GG}{CT}$ T $\frac{AA}{CC}$ C $\frac{T}{C}$ TAA (426 ~ 448 nt)	6031
R-3	T $\frac{TG}{AC}$ TC $\frac{G}{C}$ GC $\frac{AA}{G}$ T $\frac{TA}{GG}$ C $\frac{TT}{CC}$ C $\frac{C}{G}$ GCA (375 ~ 395 nt)	6032 6033

FIGURE 12



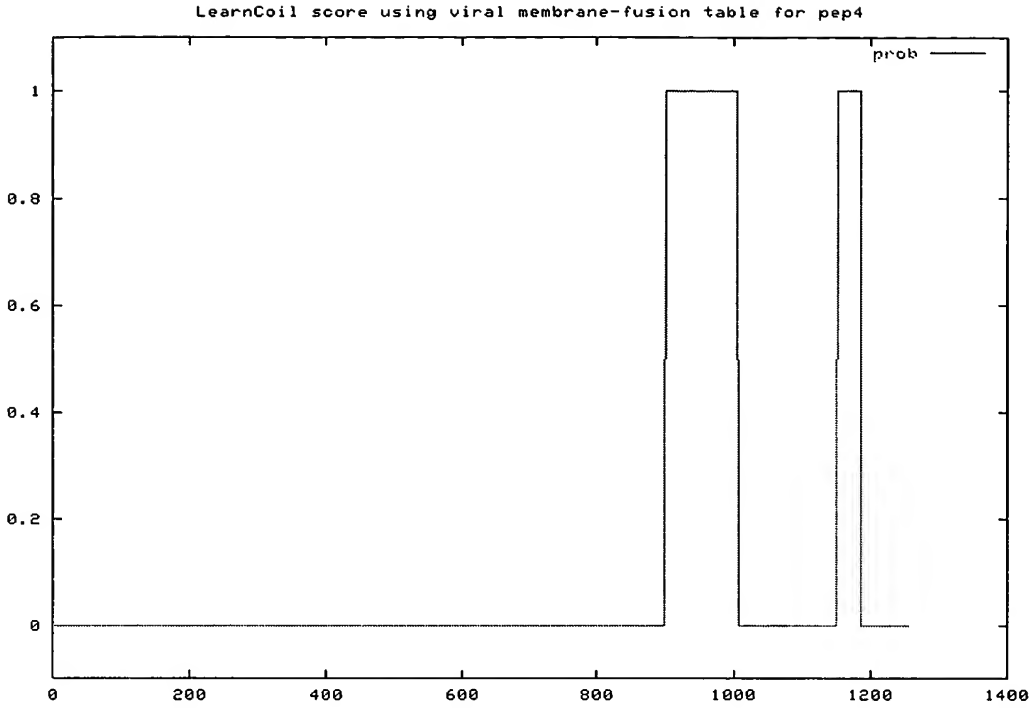


FIGURE 13

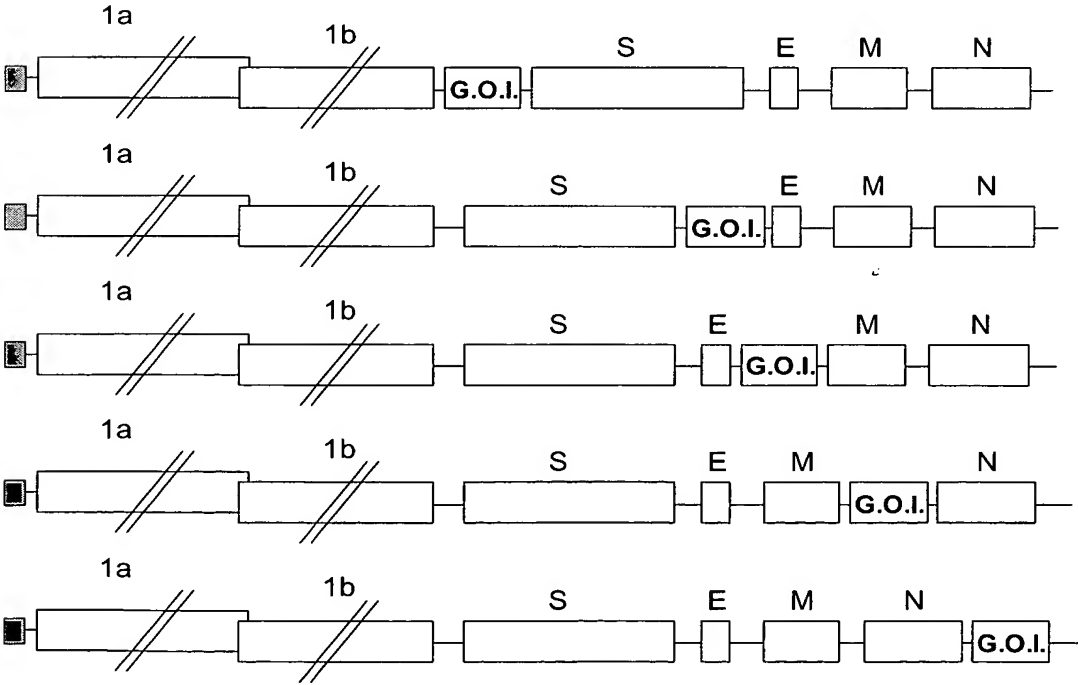


FIGURE 14

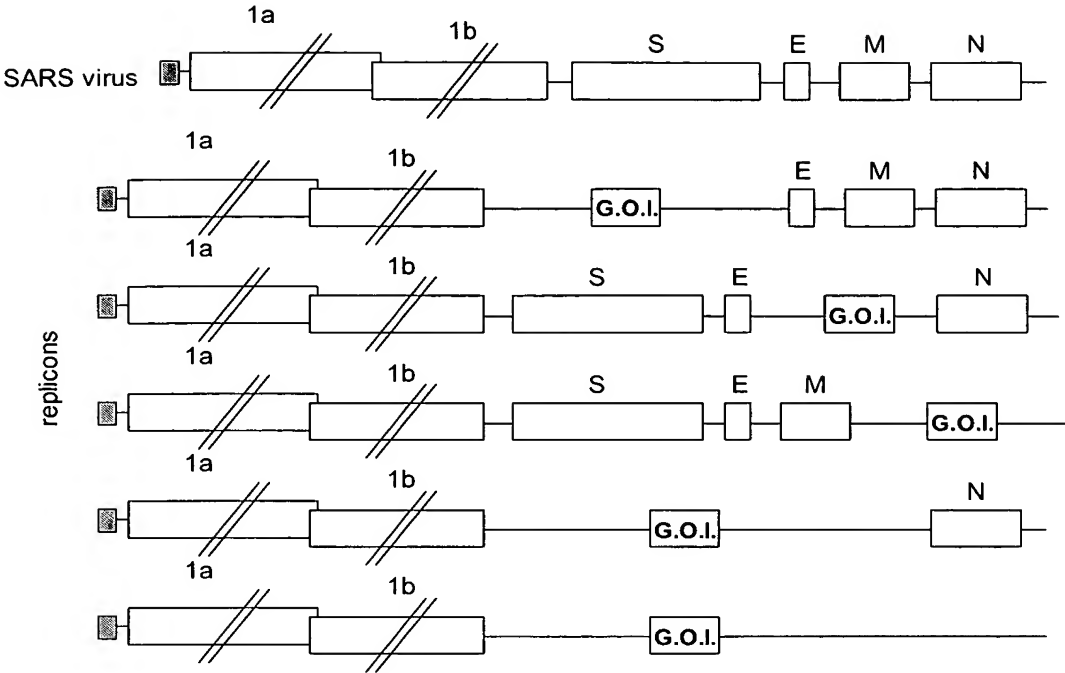


FIGURE 15

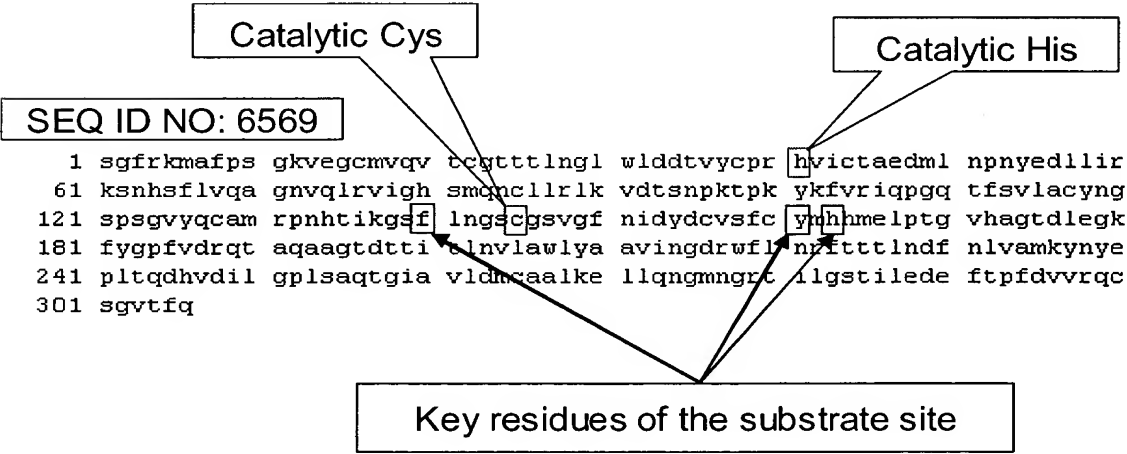


FIGURE 16

Section 1													
	(1)	1	10	20	30	40	51						
avian IBV nsp2	(1)	SGFKK	VSP	SAVEK	CIVSV	YRCNN	LNGLWLGD	YCPR	EV	G	--	KF	G
MHV nsp2	(1)	SG	VKMVSP	SKVEPC	IVSV	TYGNMT	LNGLWLDD	DKVYCPR	HVICS			DMTD	
SARS nsp2	(1)	SGFRKMAFP	GKVEGC	VQVTCG	TTTLNGLWLDD	VYCPR	HVIC	AEDMLN					
BCoV nsp2	(1)	SG	VKMVNP	SKVEPC	IVSV	TYGNMT	LNGLWLDD	DKVYCPR	HVICSA			DMTN	
Consensus	(1)	SGIVKMVSPSSKVEPCIVSVTYGNMTLNGLWLDDTVYCPRHVICSADMTN											
Section 2													
	(52)	52	60	70	80	90	102						
avian IBV nsp2	(49)	DQ	ND	LNLANNH	FEVT	QHGV	LVN	SRR	KGA	L	LQTA	ANAETPKY	
MHV nsp2	(52)	PDYP	LLCRVT	DPCV	GR	SLTVMSYQMGGC	QLVLT	TVTLQNP	TPKY				
SARS nsp2	(52)	PNYEDLLIRK	NHSFLVQAGN	VQLRV	G	SMQNC	LRLK	VDTSNP	TPKY				
BCoV nsp2	(52)	PDYT	LLCRVT	DFTV	FDR	SLTVMSYQMGGC	QLVLT	TVTLQNS	TPKY				
Consensus	(52)	PDY	NLLCRVTSSDF	VLSGR	VSLTVMSYQMGGC	LLVLT	TVTLQNP	KTPKY					
Section 3													
	(103)	103	110	120	130	140	153						
avian IBV nsp2	(100)	KFI	KANCG	FT	ACAYGG	VVGL	PVTMR	SNGTI	SS	LAG	CGSVG	N	
MHV nsp2	(102)	SFG	VVKPGETFTV	LAAYNGRPQGA	HVT	RS	HTIKGS	FLCGS	CGSVG				
SARS nsp2	(102)	KFVR	QPGQTF	VLACYNG	PSGV	QCAMP	RPNHTIKGS	LNCS	CGSVG	N			
BCoV nsp2	(102)	TFG	VVKPGETFTV	LAAYNGKPGGA	HVTMR	S	TIKGS	FLCGS	CGSVG				
Consensus	(103)	KFG	VVKPGETFTV	LAAYNGSPQGA	FHVTMR	SSHTIKGS	FLCGS	CGSVG	GFVI				
Section 4													
	(154)	154	160	170	180	190	204						
avian IBV nsp2	(151)	KGV	VNFF	M	HLELPN	LHTGTD	MG	FYGGY	VDEEVAQR	VPDNL	VTNN		
MHV nsp2	(153)	TGDSV	FVVM	M	HLEL	TGCHT	GTDFSGN	FYGPYRDAQV	QLPVQD	YDTQ	TVN		
SARS nsp2	(153)	YDCV	SFC	M	HLELP	TGVHAGTD	EGKFYGP	VDRQTAQAAGT	DTTIT	IN			
BCoV nsp2	(153)	MGDCV	FVVM	M	HLEL	TGCHT	GTDFNG	FYGPYKDAQV	QLPVQD	YIQ	VM		
Consensus	(154)	DGDCV	KFVVMHQL	ELSTG	CHTGTDL	GDFYGPYVDAQV	QLPVQD	YDTQ	TVN				
Section 5													
	(205)	205	210	220	230	240	255						
avian IBV nsp2	(202)	V	AWLYAAIISVK	ESSFSLPK	ESTTVS	ED	NKWAGD	NGCF	PFS	S	--T		
MHV nsp2	(204)	V	AWLYAAIFNRCN	----	WF	QSD	CS	E	FNWAM	NGFSS	KAD	--L	
SARS nsp2	(204)	V	AWLYAA	INGDR	----	WF	RFTT	NDFN	VAMKYN	EP	TQDHVD		
BCoV nsp2	(204)	F	AWLYAAI	NNCN	----	WF	QSDKCS	EDFNWAM	NGFSQ	K	D	--L	
Consensus	(205)	V	AWLYAAIIN	CN		WFLQSD	TCSLED	FNWAM	SNGF	SPIKSD	L		
Section 6													
	(256)	256	270	280	290	306							
avian IBV nsp2	(251)	A	TKL	MTGVDV	CKLLRTIMV	RNS	Q	GGDPIL	GQYN	FEDELTP	ESV	Q	
MHV nsp2	(247)	V	DAL	MTGV	VEQ	LAAIKRLHS	GFQ	QILGSC	FEDELTP	SDVYQ	Q		
SARS nsp2	(249)	G	PL	QQTG	AVLD	CAA	KELLQNGM	GR	TILGST	FEDEFT	PPDVVRQ		
BCoV nsp2	(247)	V	DAL	MTGV	ETLLAAIKRLKN	GFQGRQI	GSCS	FEDELTP	SDVYQ	Q			
Consensus	(256)	V	DAL	AAMTGVSVE	LLAAIKRL	S	GFQGRQILGSC	ILEDELTP	SDVYQ	Q			
Section 7													
	(307)	307	313										
avian IBV nsp2	(301)	G	V	LQ	SEQ ID NO: 6570								
MHV nsp2	(297)	L	A	G	V	K	L	Q	SEQ ID NO: 6571				
SARS nsp2	(300)	C	G	V	T	F	Q	SEQ ID NO: 6569					
BCoV nsp2	(297)	L	A	G	K	L	Q	SEQ ID NO: 6572					
Consensus	(307)	L	A	G	V	K	L	Q	SEQ ID NO: 6573				

FIGURE 17

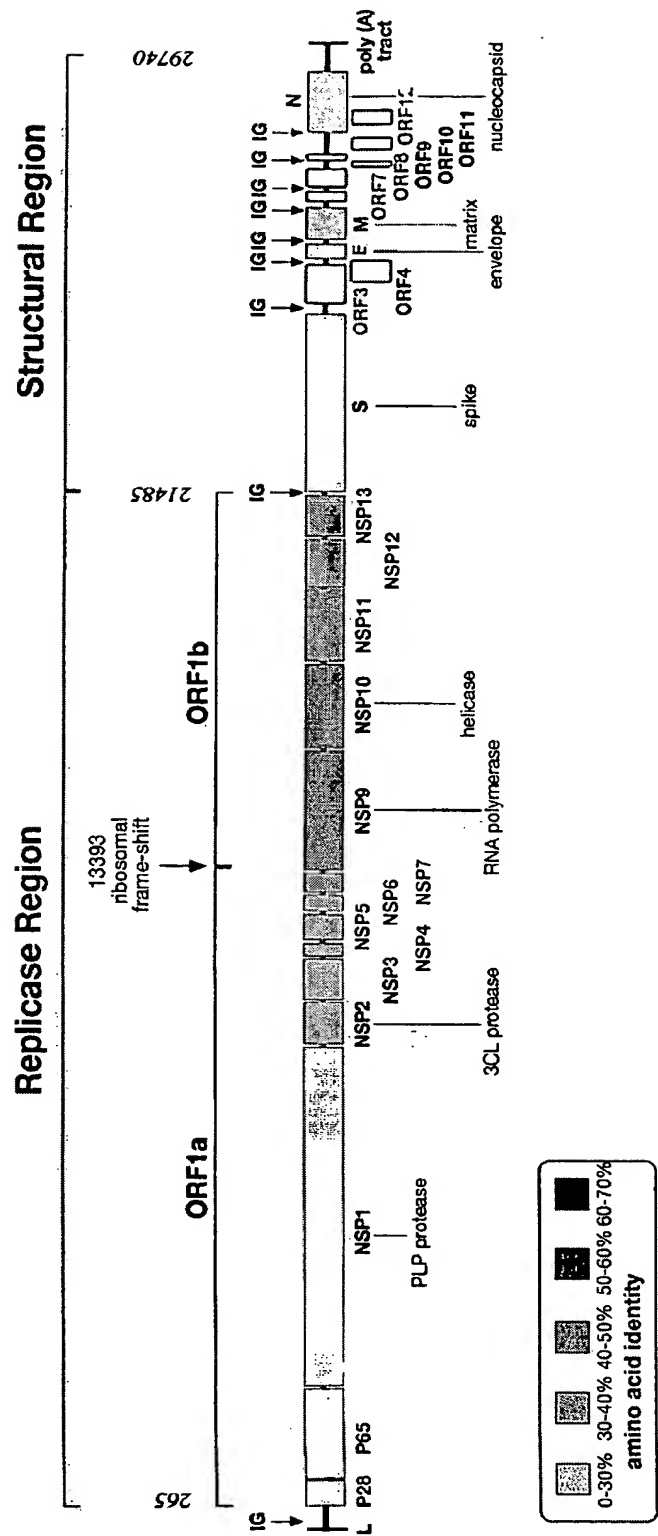


FIGURE 18

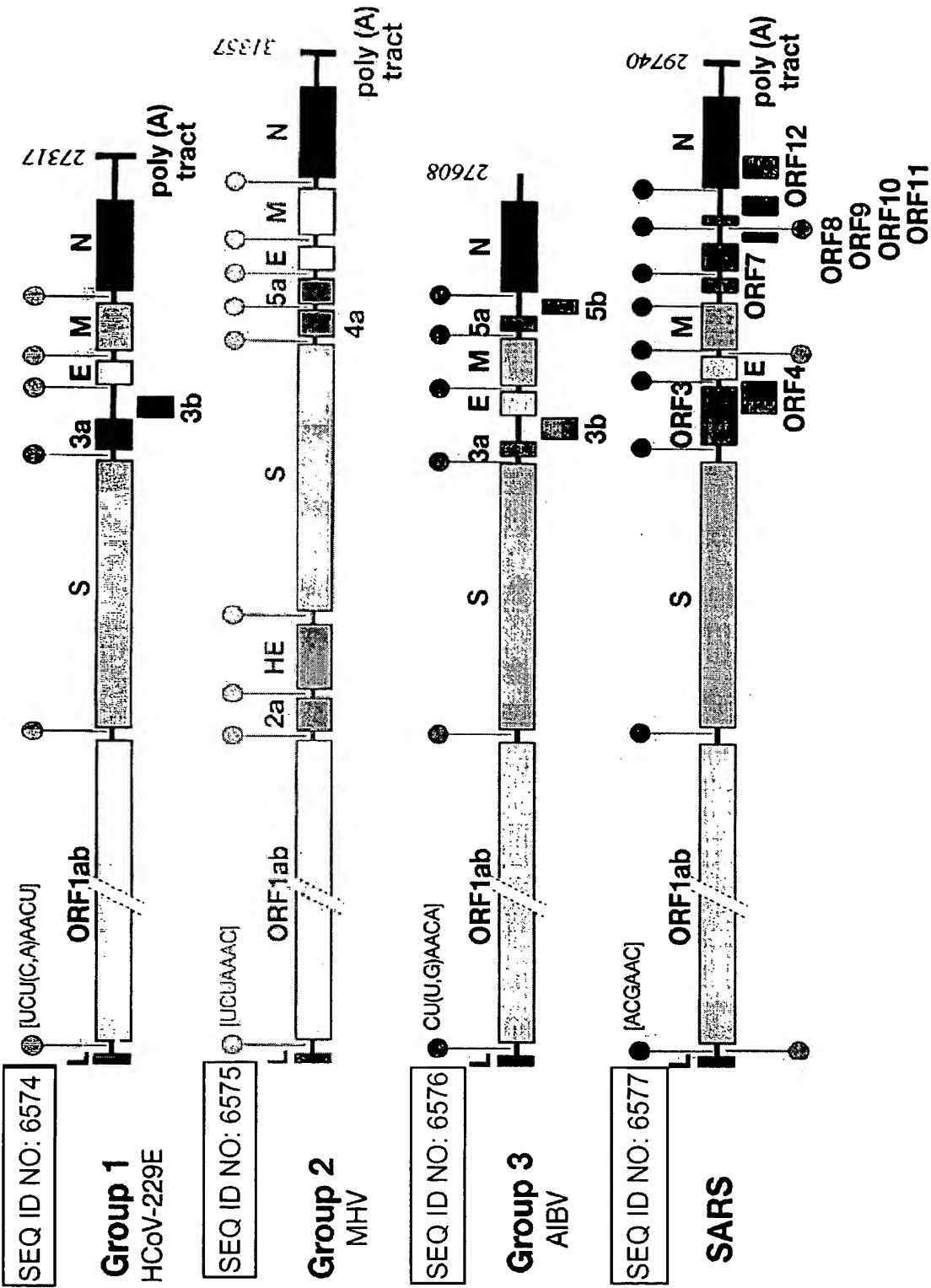


FIGURE 19

FUNCTION

STRUCTURE

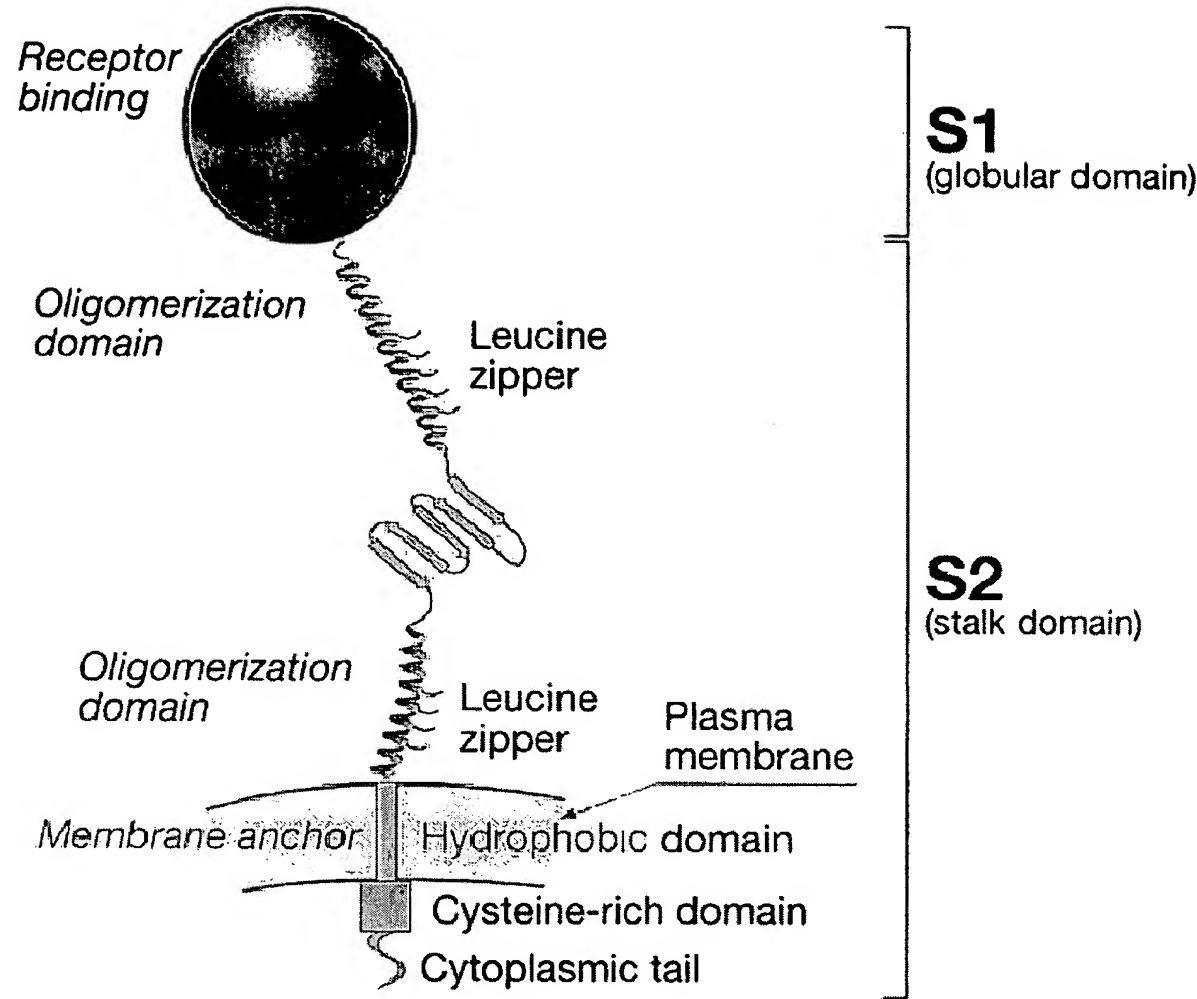


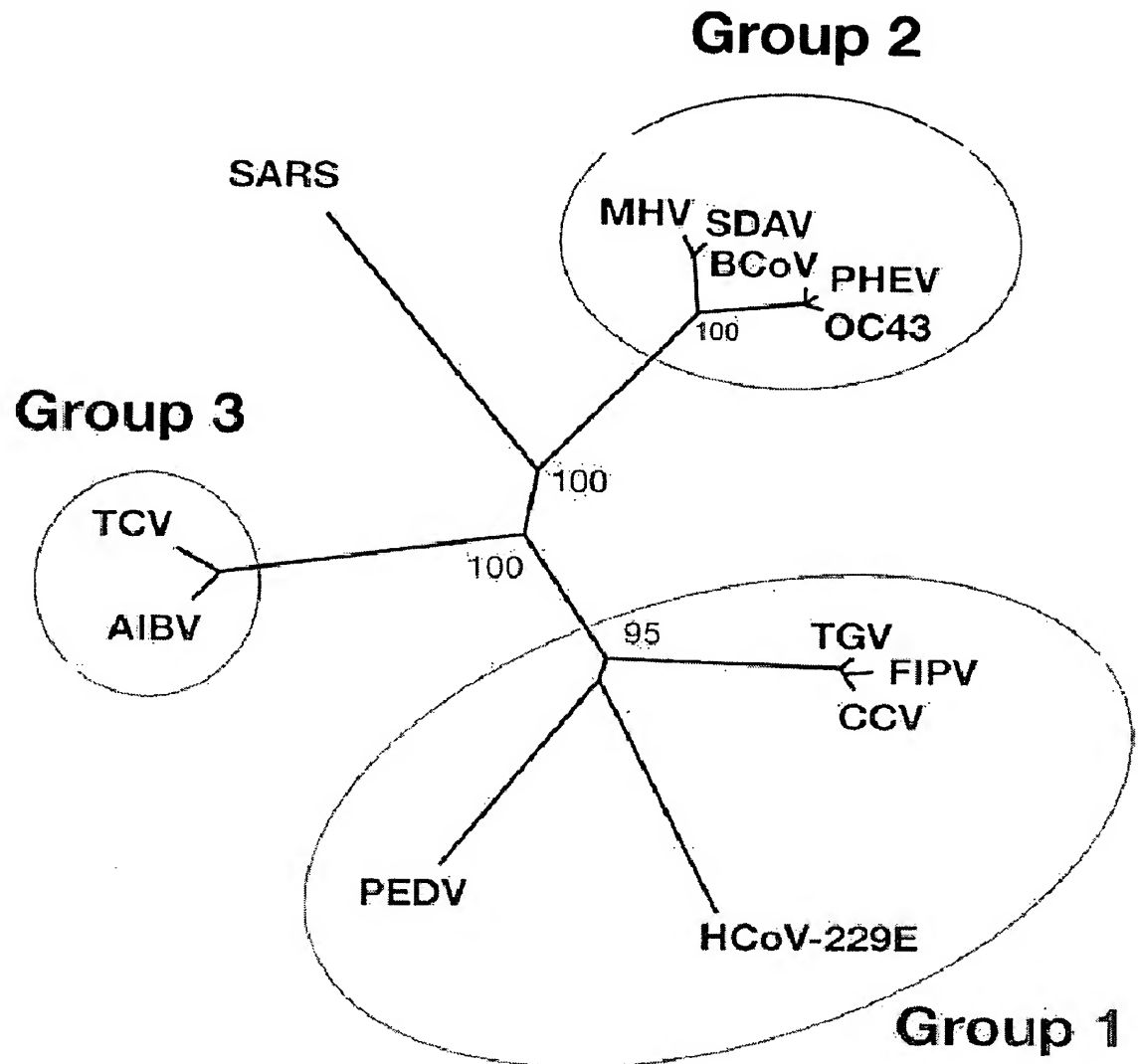
FIGURE 20

FIGURE 21

FIGURE 21A

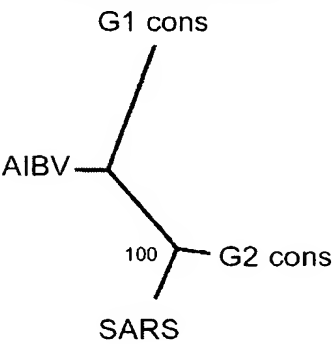


FIGURE 21B

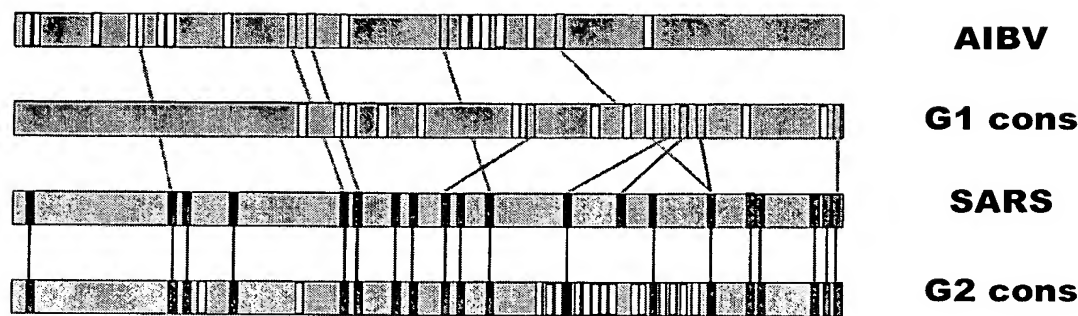


FIGURE 22

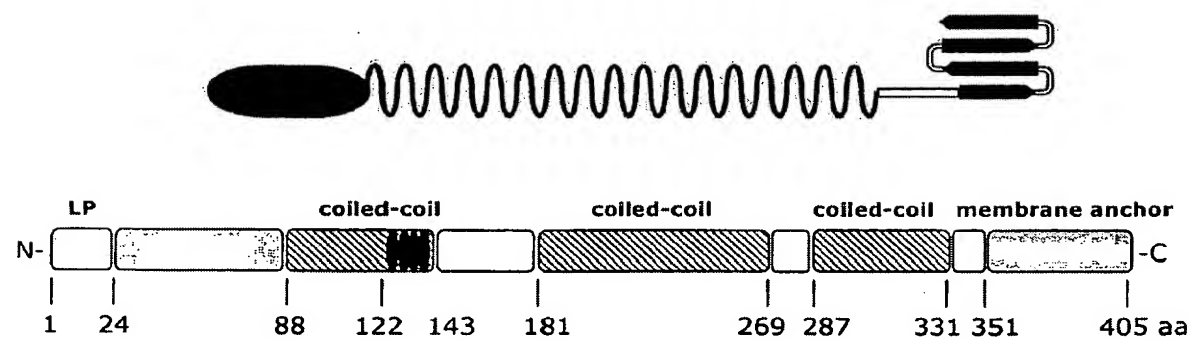


FIGURE 23

LPRKSQPTSISCRSVL-TNFKICVAVARLHA-CTYAV-TIINFTVVDKKRVTRPSSADCL
 RFRPCCSRSSAYLGFVRV-PKGKMESLVLGVNEKTHVQLSLPVLQVRDVLVRGFGDSVEE
 ALSEAREHLKNGTCGLVELEKGVLPQLEQPYVFIKRS DALSTNHGHKVVELVAEMDGIQY
 GRSGITLGLVLPVHVGETPIAYRNVLLRKNNGKAGGHSYGIDLKSYDLGDELGTDPIEDY
 EQNWNTKHGSGALRELTRELNGGAVTRYVDNNFCGPDGYPLDCIKDFLARAGKSMCTLSE
 QLDYIESKRGVYCCRDHEHEIAWFTERSDKSYEHQTPFEIKSAKKFDTFKGEC PKFVFP
 LNSKVKVIQPRVEKKKTEGFMGRIRSVYPVASPQECNNMHLSTLMKCNHCDEVSWQTCDFL
 KATCEHCGTENLVIEGPTTCGYLPTNAVVKMPCPACQDPEIGPEHSVADYHNHSNIETRL
 RKGGRTRCFGGCVFAYVGCYNKRAYWVPRASADIGSGHTGITGDNVETLNEDLLEILSRE
 RVNINIVGDFHLNEEVAIILASFSASTSAFIDTIKSLDYKSFKTIVESC GNKVKTKGKPV
 KGAWNIGQQRSVLTPLCGFPSQAAGVIRSI FARTLDAANHSIPDLQRAAVTILDGISEQS
 LRLVDAMVYTSDDLNTSVIIMAYVTGGLVQQT SQWLSNLLGTTVEKLRPIFEWIEAKLSA
 GVEFLKDAWEILKFLITGVFDIVKGQIQVASDNIKDCVKCFIDVNVKALEMCIDQVTIAG
 AKLRSLNLGEVFIAQSKGLYRQCIRGKEQLQLLMPLKAPKEVTFLEGDSHDTVLTSEEVV
 LKNGELEALETPVDSFTNGAIVGTPVCVNGLMLEIKDKEQYCALSPGLLATNNVFR LKG
 GAPIKGVTFGEDTVWEVQGYKNVRITFELDERVDKVLNEKCSVYTVESGTEVTEFACVVA
 EAVVKTLQPVSDLLTNMGIDLDEWSVATFYLFDDAGEENFSSRMYSFYPPDEEEEDDAE
 CEEEEIDETCEHEYGTEDDYQGLPLEFGASAETVRVEEEEEEDWLDDTTEQSEIEPEPEP
 TPEEPVNQFTGYLKLTDNVAIKCVDIVKEAQSANPMVIVNAANIHLKHGGGVAGALNKAT
 NGAMQKESDDYIKLNGPLTVGGSCLLSGHNLAKKCLHVVGPNLNAGEDIQLLKAAYENFN
 SQDILLAPLLSAGIFGAKPLQSLQVCVQTVRTQVYIAVNDKALYEQVVM DYLDNLKPRVE
 APKQEEPPNTEDSKTEEKSVVQKPVDVKPKIKACIDEVTTTLEETKFLT NKLLLFADING
 KLYHDSQNMLRGEDMSFLEKDAPYMGDVITSGDITCVVI PSKKAGGTTEMLSRALKKVP
 VDEYITTPGQGCAGYTLEEAKTALKKCKSAFYVLPSEAPNAKEEILGT VSWNLREMLAH
 AEETRKLMPICMDVRAIMATIQRKYKGIKIQEGIVDYGVRFFFTSKEPVASII TKLNSL
 NEPLVTMPIGYVTHGFNLEEAARCMRSLKAPAVVSVPDAVTTYNGYLTSSSKTSEEHF
 VETVSLAGSYRDWSYSGQRTELGVFELKRGDKIVYHTLES PVEFHLDGEVLSLDKLSLL
 SLREVKTIKVFTTVDNTNLHTQLVDMSMTYGGQFGPTYLDGADVTKIKPHVNHEGKTFV
 LPSDDTLRSEAFEYYHTLDESFLGRYMSALNHTKKWKFPQVGGLTSIKWADNNCYLSSVL
 LALQQLEVKFNAPALQEAYYRARAGDAANFCALILAYS NKTVGELGDVRETMT HLLQHAN
 LESAKRVLNVVCKHCGQKTTTLTGVEAVMYMGTLSDNLKTGVSI PCVCGRDATQYL VQQ
 ESSFVMMSAPPAEYKLQQGTFLCANEYTGNYQCGHYTHITAKETLYRIDGAHLTKMSEYK
 GPVTDVIFYKETS YTTTIKPVSYKLDGVTYTEIEPKLDGYKKNAYYTEQPIDLVPTQPL
 PNASFDNFKLTCSNTKFADDLNQMTGFTK PASRELSVTFFPDLNGDVVAIDYRHYSASF
 KGAKLLHKPIVWHINQATTKTTFKPNTWCLRCLWSTKPVDTSNSFEVLAVEDTQGM DNLA
 CESQQPTSEEVVENPTIQKEVIECDVKTTTEVVG NVILKPSDEGVKVTQELGHEDLMAAYV
 ENTSITIKKPNELSLALGLKTIATHGIAAINSVPWSKILAYVKPFLGQAAITTSNCAKRL
 AQRVFNNYMPYVFTLLFQLCTFTKSTNSRIRASLP TTIKNSVKSVAKLCLDAGIN YVKS
 PKFSKLFTIAMWLLLLSICLGS LICVTAAFGVLLSNFGAPSYCNGVRELYLNSSNVTTMD
 FCEGSFPCSI CLSGLDSLDSYPALETIQVTISSYKLDLTIILGLAAEWV LAYMLFTKFFYL
 LGLSAIMQVFFGYFASHFISNSWLMWFIISIVQMAPVSAMVRMYIFFASFYIWKSYVHI
 MDGCTSS TCMCYKRN RATRVECTTIVNGMKRSFYVYANGGRGFCKTHNWNCLNCDT FCT
 GSTFISDEVARDLSLQFKRPINPTDQSSYIVDSVAVKNGALHLYFDKAGQKTYERHPLSH
 FVNLDNLRANNTKGS LPINVIVFDGKSKCDESASKSASVYYSQLMCQPILLLDQALVSDV
 GDSTEVSVKMF DAYVDTFSATFSVPMEK LKALVATAHSELAKGVALDGVLSTFVSAARQG
 VVDTDVDTKD VIECLKLSHSDLEVTDGSCNNFMLTYNKVENMTPRDLGACIDCNARHIN
 AQVAKSHNVSLIWNVKDYMSLSEQLRKQIRSA AKKNNIPFRLTCATTRQVVNVIITTKISL
 KGGKIVSTCFKMLLKATLLCVLAALVCYIVMPVHTLSIHDGYTNEIIGYKAIQDGVTRDI
 ISTDDCFANKHAGFDAWFSQRGGSYKNDKSCP VVAAIITREIGFIVPGLPGTVLRAIN GD
 FLHFLPRVFSAVGNICYTPSKLIEYSDFATSACVLAAECTIFKDAMGKPVPCYD TNLLE
 GSISYSELRPDTRYV LMDGSI IQFPNTYLEGSRVRVTTFDAEYCRHGT CERSEVGICLST
 SGRWVLNNEHYRALSGVFCGV DAMNLIANIFTPLVQPVGALDVSASVAGGIIAILVTCA
 AYYFMKFRRVFG EYNHVVAANALLFLMSFTILCLVPAYSFLPGVYSVFYLYLTFYFTNDV

SFLAHLQWFAMFSPIVPFWITAIYVFCISLKHCHWFFNNYLKRKRVMFNGVTFSTFEEAAL
CTFLLNKEMYCLKRSETLLPLTQYNRYLALYNKYKYFSGALDTSYREAACCHLAKALND
FSNSGADVLYQPPQTSITSAVLQSGFRKMAFPGKVEGCMVQVTCGTTTTLNLWLDDTVY
CPRHVICTAEDMLNPYEDLLIRKSNHSFLVQAGNVQLRVIGHSMQNCLLRLKVDTSNPK
TPKYKFVRIQPGQTFSVLACYNGSPSGVYQCAMPNHTIKGSFLNGSCGSGVFNIDYDCV
SFCYMHMELPTGVHAGTDLEGKFYGPFDVDRQTAQAAGTDTTITLNLAWLYAAVINGDR
WFLNRFTTTLNDENLVAMKYNYEPLTQDHVDILGPLSAQTGIAVLDMCAALKELLQNGMN
GRTILGSTILEDEFTFPFDVVRQCSGVTFQGKFKKIVKGTHHWMLLTFLTSLLIILVQSTQW
SLFFFVYENAFLPFTLGIMAIAACAMLLVKHKAFLCLFLLPSLATVAYFNMVYMPASWV
MRIMTWLELADTSLSGYRLKDCVMYASALVLLILMTARTVYDDAARRVWTLNMVITLVYK
VYYGNALDQAI SMWALVISVTSNYSGVVTTIMFLARAI VFCVEYYPLLFITGNTLQCIM
LVYCFGLGYCCCCYFGLFCLLNRYFRLTLGVYDYL VSTQEF RYMNSQGLLPPKSSIDAFKL
NIKLLGIGGKPCIKVATVQSKMSDVKCTSVVLLSVLQQLRVESSSKLWAQCVQLHNDILL
AKDTTEAFEKMSVLLSVLLSMQGAVDINRLCEEMLDNRATLQAIASEFSSLP SYAAYATA
QEAYEQAVANGDSEVVLKLLKKS LNVAKSEFDRDAAMQRKLEKMAQAMQMYKQARSED
KRAKVT SAMQTM LFTMLRKL DNDALNNI INNARDGCVPLNI I PLTTAAKLMVVVPDYGT
KNTCDGNTFTYASALWEIQQVVDADSKI VQLSEINMDNSPNLAWPLIVTALRANSVAVKLQ
NNELSPVALRQMSCAAGTTQTACTDDNALAYNNSKGGRFVLALLSDHQDLKWARFPKSD
GTGTIYTELEPPCRFVTDTPKGPKVKYLYFIKGLNNLNRGMVLGSLAATVRLQAGNATEV
PANSTVLSFCAFAVDPAKAYKDYLASGGQPITNCVKMLCTHTGTGQAITVTPEANMDQES
FGGASCCLYCRCHIDHPNPKGFCDLKGKYVQIPTTCANDPVGFTLRNTVCTVCGMWKGYG
CSCDQLREPLMQSADASTFLNGFAV-VQPV LHRAAQALV LMSSTGLLI FTTKKLLVLQSS
-KLI AVASRRMRKAIY-TLTL-LRGILCLTTNMKRLFITWLKIVQRLLSMTFSSLE-MV
TWYHIYHVS-VNTQWLI-SMLYVILMRVIVIH-KKYSSHTIAVMMIISIRRIGMTS-RI
LTSYAYMLT-VSVYANYH-RLYNSAMLCVMQAL-AY-H-IIRILMGTTGTISVISYK-HQA
AEFLLWIHITHC-CPSSL-LGHWLLSPIWMLISQNHLLSGIC-NMILRKRDFVSSTVILN
IGTRHTIPIVLTVMIGVSFIVQTLMCYFLLCFHLQVLDH--EKYL-MVFLLLFQLDITF
VS-ESYIIRM-TYIARVSVRNF-CMLLIQLCMQLLAIYC-INALHAFQ-LH-QTMLLFK
LSNPVILIKTFMTLLCLKVSLRKEVLLN-NTSSLLRMATLLSVIMTIIVIICQQCVISDN
SYS-LKLLINTLIVTMVAVLMPTK-SLTIWINQLVSHLINGVRLDFIMTQ-VMRIKMHS
RILSVMSLL-LK-ILSMPLVQRIELAP-LVSLSVVL-QIDSFIRNY-SQ-PPLEELLW-
LEQASFTVAGIIC-KLFTVM-KLHTLWVGIIQNVTEPCLTCLG-WPLLFLLANITLAVTY
HTVSTG-LTSVRKY-VRWSCVAAHYMLNQVEHHPVMLQLLMLIVSLTFVKLLQPM-MHFF
QLMVIR-LTMSAIYNTGSMVSIEIGMLIMNSWMSFTLTVCVNISP--FFLMPLCAITV
TMRLKV--LALRTLQOFFIIKIMCSCLRQNVGLRLTLTKDLTNFAHSIQC-LNKEMITCT
CLTQIHQEY-AQAVLSMILSKQMVHL-LKGSCHWLLMLTHLQNILIRSMMSFTCIYNTL
ESYMSLLATCWTICIP-C-LMITPHGTGNLSFMRLCTHHIQSCRL-VLVYCAIHRHLHFA
VPVLGDHSYVASAAMTMSFQHHTN-CCLLIPMFAMPQVVMVSLM-HNCI-EV-AIIASHIS
LPLVFHYVLMVRFLVYTKTHV-AVTMSLTSMR-QHVIGLMLAITYLPTLVLRDSSFSQOK
RSKPLRKHLSCHEVLRHTS-MLVITLC-HLTL-CHLVHLL-CHKSTM-ELLACTQHS
TSQMSFLAMLQIIKRSACKSTLHSHKDLHLVVRVILPSDLLSITHLLA-CIRHALMQLLMP
YVKRH-NICP-INVESYLRVRA-SVLINSK-IQH-NSMFSAL-MHCQKQLLTL-SLMKS
LWLLIMT-VLSMLDFVQNTTSILAILLNYQPPAHC-LKAH-NQNILIQCADL-KQ-VQTC
SLELVAVVLLKLLTL-VL-FMTIS-KHTRISQLNASKCSTKVLLHMMFHLQSTD LK-AL-
ENFLHAILLGEKLFLSHLIIHRTL-LQKS-DCLRLLIHRVNLNMTMSYSHKLLKQHTLV
MSTASMWLSQGQKLAFCAL-CLIEIFMTNCNLQV-KYHVAMWLHYKQKM-LDFLRTVVRSL
LVFILHRHLHTSALI-SSRLKDYVLTYQAYQRT-PTVDSSL-WVSK-ITKSMVTLICLSP
AKKLFVTFVRGLALM-RAVMQLEMLWVLTYLSS-DFLQVLT--LYRLVMLTLKITQNSPE
LMQNLHQVTSNLILYHSCIKACPGM-CVLR-YKCSVIH-KDCQTESCSSFGRMALS LHQ-
STLSRLDLKERVVCVTNVQLAFLHQILMPAGIILWVLTMSITHL-LMFSSGALRVTRV
TMTNIARYMEMHMLVVMLS-LDV-QSMSALLSALIGLLNTLL-EMN-GLILLAKEYNTW
L-SLHCLLISFQFFMTLEIQR LSSVCLRLK-NGSSTMLSHVVTKLTK-RNSSILMLHITI
NSLMVFVFCGIVTLIVTQPMQLCVGLTQESCQT-TYQAVMVVCM-ISMHSTLQLSIKVH
LLI-SNCLSFTILIVLVSLMANK-CRILIMFHSNLLRVLHDAI-VVLFADTMQMSTDSTW

MHII--FLDLAYGFTNNLILITCGIHLPGYRV-KMWLIMLLIKDTLMDTPAKHLFPSLI
MLFTQR-MVLMWRSLKIRQHFLMLHLSFGLSVTLNQCQRLRYSIIWVLISLLIL-SGTT
KEKPQHMYLQ-VSAQ-LTLPRNLLRVLVHLHLSCLMVEWKDR-TFLETPVMVF--QKVQS
KV-HLQRDQHKLASMESH-LENQ-KHSLTTLRK-TALFNSCLKPTLLRAET-RILSPDHK
WKLTFSSSLWMNSYSDISSRAMPSNTSFMEISVMDNLAVFI--A-PSAHKIHHLN-RIL
SLWTAQ-KITS-QMRKQVHQNVCVL-LIFYLMTLSR--SHKICQ-FQKWSRLQLTMLKFH
SCFGVRMDMLKPSTQNYKQVERGNQVLRCLTCTRCKEFLKSVTFRIMVKMLLYQKE---
MSQSILNCVNT-IHLL-LYPTT-ELFTLVLALIKELHQVQLCSDNGCQLAHYLSIQILMT
SSPTHILL-LETVQQYIRLINGTLLLAICMTLGPNM-QKRMTLKKGFSLICVDL-SKN-P
WVVL-L-R-QSILGMLTFTSLWAISHGGQLLQM-MHHHRKHF-LGLTILASRRNKLMAI
PCMLTTFSGGTQILSSCLPIHSLT-ANFLN-EELL-CLLRRIKSMI-FILFWKKVGLSL
EKTTELWFQVIFLLTTKRTCLFSYFLLSLVVVTLTGAPLLMMFKLLITLNLHL-GGFT
ILMKFLDQTLFI-LRIYFFHFILMLQGFILLIIRLATLSYLLRMVFILLPQRNQMLSVVG
FLVLP-TTSHSR-LLLTILLMLLYEHVTLNCVTTLSSLFLNPWVHRHIL-YSIMHLIALS
STYLMFPRLMFQKSQVILNTYESLCLKIKMGFSMFIRAINL-M-FVIYLLVLT-LNFLS
CLLVLTQLILEPFLQPFHLLKTFGARQLQPILLAI-SQLHLCSSMMKMVQSQMLLIVLKI
HLLNSNALLRALRLTKEFTRPLISGLFPQEML-DSLILQTCVLLERFLMLLSLSMHGR
EKKFLIVLLITLCSTTQHFFQPLSAMAFLPLS-MIFASPMQMILL-SREMM-DK-RQDK
LVLLLIIIINCQMISWVVSLLGILGTLMLLQLVIIIIINIGILDMASLGPLRETYLMCLSP
LMANLAPHLLLIVIGH-MIMVFTPLLALATNLTEL-YFLLNF-MHRPRFVDQNYPLTLR
TSVSILILMDSLVLVC-LLLQRDFNHFNNLAVMFLISLIPFEILKHLKY-TFHLALLGV-
V-LHLEQMLHLKLLFYIKMLTALMFLQQFMQINSHQLGAYILLETMYSRLKQAVL-ELSM
STLLMSATFLELAFVLVTIQFLYVVLAKNLLWLILCL-VLIVQLLTLITPLLYLLTFQ
LALLQK-CLFLWLKPP-IVICTSAEILLNVLICFSNMVAFAHN-IVHSQVLLLNRIATHV
KCSLKSNNKCTKPQL-NILVVLIFHKYYLTL-SQLRGLLLRTC SLIR-HSLMLAS-SNMAN
A-VILMLEISFVRRSSMDLQCCHLCSLMI-LLPTLLL-LVVLPLLDGHVLVALLFKYLL
CKWHIGSMALELPKMFSMRTKNKSPTNLTRRLVKFKNHLQHQHQLHWASCKTLLTRMLKH-
THLLNNLALILVQFQVC-MISFRDLIKSRRRYKLTG-LQADFKAFKPM-HNN-SGLLKS
LLLILLLLKCLSVFLDNQKELTFEVRATTLCPSHKQPRMVLSSYMSRMCHPRRGTSPQRQ
QFVMKAKHTSLVKVFLCLMALLGLLHRGTSFLHK-LLQTIHLSQEIVMSLLASLTQFMI
LCNLSLTHSKKSWTSTSKIHHQMLILATFQALTLLSSTFKKKLTASMRSLKI-MNHSLT
FKNWENMSNINLGLMFGSASLLD-LPSSWLQSCFVA-LVVAVASRVHALVLAASLMRM
TLSQFSRVSNYITHKRTYGFVYEIFYSWINYCTASKN-QCFSCKYCSCYSNDTATSLTPF
RMACYWRCISCCFSERYQNNCAQ-KMAASPL-GLPVHLQFTAAICYHLFTSFACRCRYGG
AIFVPLCLDIFSTMHQRM-NYYEMLALLEVQIQEPITL-CQLLCLLAHT-L-LLYTI-QC
HRYNCRY-R-RHFNKTQRRLPNWWLF-G-ALRC-RLCRCTWLFHRSLLPA-VYTNYRH
WY-KCYILHL-QAC-RPTECANTHNRRFLRSC-SSNGSNL--ADDDY-RAFVSTRK-VRT
YVLIRFGRNRYVNS--RTSFSCFRGILASHTSHPYCASIVCVLLQYC-REFSKTNGRLRL
AC-KSELF-RSS-SSGLNELTIIIIIFGTLTLLIMADNGTITVEELKQLEQWNLVIGFL
FLAWIMLLQFAYSNNRFLYIIKLVFLWLLWPVTLACFVLAAYRINWVTGGIAIAMACI
VGLMWLSYFVASFRLFARTRSMWSFNPETNILLNVPLRGITVTRPLMESELVIGAVIIRG
HLRMAGHSLGRCDIKDLPKEITVATSRTLSYKLGASQVRGTDSGFAAYNRIRIGNYKLN
TDHAGSNDNIALLVQ-VTTDVSSC-LPGYNSRDIDYHYEDFQDCYLES-RYNKFNSSETII
-ASN-EELFGVR--RTYGVRLSIKRT-KLFSS-H-LYLHLASYITIRSVLEVRLYY-KNL
AHQEHTRAIHHFTLLLTLNLH-LALAHTLLLVLTVLDIPISCVQDQFHQNFSSDKRRFN
KSSTRHFFSLLLL-YF-YFASPLRERQNE-AHFN-LLFVLFSLSAIPCFNNAYYILVFTR
NPGSRRTLYQSLNEHETSHCFDLYFSMQLHMHCSALCI--TSCA-RSL-GTTLGVLIA
LLGFVL-ERFYLFIDGTLWFKHAHMLLSTVVKIQLVVRL-LGVGTFMKVTKLLHLETYLL
F-INEQIKMSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQGLPNNTAS
WFTALTQHGKEELRFPRGQGVPIINTNSGPDDQIGYYRRATRVRGGDGKMKELSPRWYFY
YLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNNAATVLQLPQGTTLPKGF
YAEGSRGGSQASSRSSRSRGNSTPGSSRGNSPARMASGGGETALALLLLDRLNQLE
SKVSGKGQQQQGQTVTKKSAAEASKKPRQKRTATKQYNVTQAFGRRGPEQTQGNFGDQDL
IRQGTDYKHPQIAQFAPSASAFFGMSRIGMEVTPSGTWLTYHGAIKLDDKDPQFKDNVI
LLNKHIDAYKTFFPTEPKKDKKKKTDEAQPLPQRQKKQPTVTLLPAADMDDFSRQLQNSM

SGASADSTQA-TLMMTTQGRWAM-TFSQFRLRYIVYSCAE-ILVTKQHK-V-LTLISHSN
L-SMCNIREDLKEPPHFHRGHAHEYDRGYSE-C-GELPIWKSPNV-N-F-CYPHVILIAS

FIGURE 24

TQEKPTNLDLL-ICSLNEL-NLCSRSAACLVHLRSINNNKFYCR-QETSNSSLFCRLLT
 VSSVLQSIISIPRFRPGVTER-DGEPCSWCQRENTTRPTQFACPSG-RRASAWLRGLCGRG
 PIGGT-TPQKWLWSSRAGKRRTAPA-TALCVH-TF-CLKHQSRPQGR-AGCRNGRHSVR
 S-RYNTGSTRATCGRNPNCIPQCSSS-ER--GSRWS-LWHRSKVL-LR-RAWH-SH-RL-
 TKLEH-AWQWCTP-THS-AQWRCSHSLCRQQFLWPRWVPS-LHQRFSTRGQVNVHSFRT
 T-LHRVEERCLLLP-P-A-NCLVH-AL--ELRAPDTRLN-ECQEI-HFQRGMPKVCVSS-
 LKSQSHSTTC-KEKD-GFHGAYTLCVPCCISTGV-QYALVYLDDEM-SLR-SFMADVRLSE
 SHL-TLWH-KFSY-RTYYMWVPTY-CCSENAMSCLSRPRDWT-A-CCRLSQPLKH-NSTP
 QGR-D-MFWRLCVCLCWLL--ACLLGSSC-C-YWLRPYWHYW-QCGDLE-GSP-DTES-T
 C-H-HCWRFSFE-RGCHHFGIFLCFYKCLY-HYKES-LQVFQNH-C-VLR-L-SYQGKARK
 RCLEHWTTEISFNNTTVWFSLTGCWCYQINFCAHT-CSKPLNS-FAKSSCHHT-WYF-TVI
 TSCRRHGLYFRPAHQQCHYYGICNWWSCCTTDFSVVV-SFGHYC-KTQAYL-MD-GET-CR
 S-ISQGLGDSQISHYRCF-HRQGSNTGCFR-HQGLCKMLH-CC-QGTRNVH-SSHWR
 KVAITQLR-SLHRSKQGTLPSTVYTQGAATTHAS-GTKRSNLS-R-FT-HSTYL-GGCS
 QER-TRSTRDAR--LHKWSYRRHTSLCKWPHALRD-GQRTILRIVSWFTGYKQCLSLKRG
 CTN-RCNLWRRYCLGSSRLQECENHI-A--TC-QSA--KVLCLHC-IRYRSY-VCMCCSR
 GCCEDFTTSF-SPYQHGY-S--VECSYILLI--CW-RKLFITYVLFLLPSR-GRRGRCRV
 -GRRN--NL-T-VRYRG-LSRSPSGIWCLS-NSSS-GRRRGRLAG-YY-AIRD-ARTRTY
 T-RTS-SVYWLFKTY-QCCH-MC-HR-GGTKC-SYGDCKCC-HTPETWWWCSRCTQQGNQ
 WCHAKGE--LH-AKWPSYSRRVLFAPWT-SC-EVSACCWT-PKCR-GHPAS-GSI-KFQF
 TGHILTCTIVSRHIWC-TTSVFTSVRADGSYTGLYCSQ-QSSL-AGCHGLS--PEA-SGS
 T-TRGATKHRRFQN-GEICRTEACRCEAKN-GLH--GYHNTGRN-VSYQ-VTLVC-YQW-
 ALP-FSEHA-R-RYVFP-EGCTLHGR-CYH-W-YHLCNTLQKGWWHY-DALKSFEEAS
 --VYNHVPWTRMCWLYT-GS-DCS-EMQICILCTTFRST-C-GRDSRNCILEFERNACSC
 -RDKKINAYMHGC-SHNGNHPT-V-RN-NSRGHR-LWCPILLY--RACSFYYEAEISK
 -AACHNANWLCDTWF-S-RGCALYAFS-SSCRSVSIITRCCYI-WIPHFVIKDI-GALC
 RNSFFGWLQLRVLFRAYRVRC-IS-AW-QNCVPHSGEPRRVSS-R-GSFT-QTKESLI
 PAGG-DYKSVHNCQGH-SPHTACGYVYDIWTAVWSNILGWC-CYKN-TSCKS-G-DFLCT
 T---HTT--SFRVLPYS--EFSW-VHVCFKPKHEMIEISSWWFNFN-MG--QLLFV-CFI
 STSTA-SQIQCTSTSRGLL-SPCW-CC-LLCTHTRLQ--NCWRAW-CQRNYDPSSTAC-F
 GICKASS-CGV-TLWSENYYLNGCRSCDVYGYSL--S-DRCFHSMCVWS-CYTISSTTR
 VFFCYDVCTTC-V-ITARYILMCE-VHW-LSVWSLHSYNC-GDPLSY-RSSPYKDVRVQR
 TSD-CFLQGNILHYNHQACVV-TRWSYLHRD-TKIGWVL-KG-CLLYRAAYRPCTNSTIT
 KCEF--FQTHMF-HKIC--FKSNDRLHKASFTRAICHILPRLEWRCSGY-L-TLFSEFQE
 RC-ITA-ANCLAH-PGYNQDNVQTKHLVFTLSLEYKASRYFKFI-SSGSRHTRNGQSCL
 -KSTTHL-RSSGKSYHTEGSHRV-RENYRSCRQCHT-TIR-RC-SNTRVRS-GSYGCLCG
 KHKHYH-ET--AFTSLRKFNNCHSWYCCN--CSLE-NFGLCQTLIRTSSNYNIKLR-EIS
 TTCV-QLYALCVYIIVPIVYFY-KYQF-N-SFTTYNYC-K-C-ECC-IMFGCRH-LCEVT
 QIF-IVHNRYVAIVVKYLLRFSNLCNCCFWCTLI-FWCSFLL-WR-RIVS-FV-RYYYGF
 L-RFFSLQHLFKWIRLP-FLSSS-NHSGDDFIVQARLDNFRSGR-VGFGIYVVKILLFI
 RSFSYNAGVLWLF-C-SFHQQFLAHVVYH-YCTNGTRFCNG-DVHLLCFFLLHMEELCSYH
 GWLHLFDLHDVL-AQSCHTR-VYNYC-WHEEIFLCLCKWRPWLLQDSQLELSQL-HILHW
 -YIH---SCS-FVTPV-KTNQPY-PVIVYC--CCCEKWRASPLL-QGWSKDL-ETSALPF
 CQFRQFES-QH-RFTAY-CHSF-WQVQMRRVCF-VCFCVLQSAADVPTYSA-PSSCIRR
 R-Y-SFR-DV-CLCRHLFSNF-CSYGKT-GTCCYSSQRVSKGCSFRWCFFYIRVSCPTRC
 C-YRC-HKGCY-MSQTFTSL-LRSDR-QL-QFHAHL--G-KHDAQRSWRMY-L-CKAYQC
 PSSKKSQCFTHLECKRLHVFI-TAA-TNS-CCQEEQHTF-TNLCYN-TGCQCHNY-NLTQ
 GW-DC-YLF-TYA-GHIIVRSCCIGLLRYASTYIVNP-WLHK-NHWLQSHSGWCHS-HH
 FY--LFCK-TCWF-RMV-PAWWFIQK-QKLPCSSCYHYKRDWFHSAWLTGYCAESNQW-L
 LAFSTSCF-CCWQHLLHTFQTH-V--FCYLCLRSCC-VYNF-GCYGQTCAILL-H-FARG
 FYFL--ASSRHSLCAYGWFHHTVS-HLPGGFC-SSNNF-C-VL-TWYMRKVRSRYLPIYQ
 W-MGS---ALQSSIRSFLWC-CDESHS-HLYSSCATCGCFRCVCFSSGWYYCHIGDLCC
 LLLYEIQTCFW-VQPCCCC-CTFVFDVFHYTSLGTSLSQLSAGSLLSLLLVLDFHQC-CF

ILGSPSMVCHVFSYCAFLDNSNLCILYFSEALPLVL-QLS-EKSHV-WSYI-YLRGGCFV
YLFAQQGNVPKIA-RDTVATYTV-QVSCSI-QVQVFQWSLRYYQLS-SSLLPLSKGSK-L
-QLRC-CSLPTTTDINHFCSSAEWF-ENGIPVRQS-RVHGTSNLWNYNS-WIVVG-HSIL
SKTCHLHSRRHA-S-L-RSAHSQIQP-LSCSGWQCSTSCYWPFYAKLSA-A-S-YF-P-D
TQV-ICPYPTWSNIFSSSMLQWFTIWCLSVCHET-SYH-RFFP-WIMW-CWF-H-L-LRV
FLLYASYGASNRSTRWY-LRR-ILWSIC-QTNCTGCRYRHNHNKICFGMAVCCCYQW--V
VS--IHHYFE-L-PCGNEVQL-TFDTRSC-HIGTSFCSNRNCRRLRYVCCFERAAAEWYEW
SYYPW-HYFRR-VYTI-CC-TMLWCYLPR-VQENC-GHSSLD AFNFLDITIDSCSKYTVV
TVFLCLRECFLAIYSWYYGNCCMCYAAAC-A-ARILVLVSVTFSCNSCLL-YGLHAC-LGD
AYHDMA-IG-H-LVWL-A-GLCYVCFSSFAYSHDSSHCL--CC-TCLDTDECHYTCLQS
LLW-CFRSSYFHVGLSYFCNL-LFWCRYDYHVFS-SYSVCVC-VLPVIYYWQHLYTVYHA
CLLFLRLLLLLLLLLWPFLETOPLLQAYSWCL-LLGLYTRI-VYELPGAFAS-E-Y-CFQA-
H-VVGYWR-TMYQGCYCTV-NV-RKVHICGTALGSST-SRVIF-IVGTMCTTPQ-YSSC
KRHN-SFREDGFSFVCFAIHAGCCRH--VVRGNAR-PCYSSGYCFRI-FTTIIICRLCHCP
GGL-AGCS-W-F-SRSQKVKEIFECG-I-V-P-CCHATQVGKDGRSGYDPNVQTGKI-GQ
EGKSN-CYANNALHYA-EA---CT-QHYQQCA-WLCSTQHHTIDYSSQTHGCCP-LWYLQ
EHL-W-HLYICICTLGNPASC-CG-QDCST--N-HGQFTKFGLASCYSSKSQSLSC-TTE
--TESSSTTTDVLGWHYHTNSLY--QCTCLL-QFEGR-VCAGITIRPPRSQMG-IP-E-W
YRYNLHRTGTTL-VCYRHTKRA-SEILVLHQRLKQPK-RYGAGQFSCYSTSSGWKCYRST
CQFNCAFLLCFCSRPC-SI-GLPSKWRTTNHQLCEDVVYTHWYRTGNYCNTRS-HGPRVL
WWCFMLSVL-MPH-PSKS-RIL-LER-VRPNTYHLC--PSGFYT-KHSLYRLRNVERLWL
-L-PTPRTLDAVCGCINVFKRVCVSAARLTPCGTGTSTDVVYRAFDIYNEKVAGFAKFL
KTNCCRFQEKDEEGNLLDSYFVVKRHTMSNYQHEETIYNLVKDCPAVAVHDFFKFRVDGD
MVPHISRQRLTKYTMADLVYALRHFDENCDTLKEILVTYNCCDDDDYFNKKDWYDFVENP
DILRVYANLGERVRQSLLKTQVQFC DAMRDAGIVGVLTLDNQDLNGNWDYDFGDFVQVAPGC
GVPIVDSYSSLLMPILTLTRALAAESHMDADLAKPLIKWDLKYDFTEERLCLFDRYFKY
WDQTYHPNCINCLDDRCILHCANFNVLFSTVPPTSFGLVRKI FVDGVPFVSVSTGYHFR
ELGVVHNQDVNLHSSRLSFKELLVYAADPAMHAAAGNLLLDKRTTCFSAALTNNAVQOT
VKPGNFNKDFYDFAVSKGFFKEGSSVELKHFFAQDGNAAISDYDYRYNLPTMCDIRQL
LFVVEVVDKYFDCYDGGCINANQVIVNNLDKSAGFPFNKWGKARLYYDSMSYEDQDALFA
YTKRNVIPITITQMNLYAISAKNRARTVAGVSICTMTNRQFHQKLLKSIAATRGTAVVI
GTSKFYGGWHNMLKTVYSDVETPHLMGWDPKCDRAMPNMLRIMASLVLARKHNTCCNLS
HRFYRLANECAQVLSEVMCGGSLYVKPGGTSSGDATTAYANSVFNICQAVTANVNALLS
TDGNKIADKYVRNLQHRLYECLYRNRDVEHFEVDEFYAYLRKHFSMMILSDDAVVCYNSN
YAAQGLVASIKNEKAVLYYQNNVFMSEAKCWTETDLTKGPHEFCSQHTMLVKQGDDYVYL
PYPDPSRI LGAGCFVDDIVKTDGTLMIERFVSLAIDAYPLTKHPNQEYADV FHLYLQYIR
KLHDELTGHMLDMYSVMLTNDNTSRYWEPEFYEAMYTPHTVLQAVGACVLCNSQTS LRCG
ACIRRPFLCCKCCYDHVISTSHKLVLVSNPYVCNAPGCDVTDVTQLYLGMSY YCKSHKP
PISFPLCANGQVFGLYKNTCVGSDNVTDFNAIATCDWTNAGDYILANTCTERLKLFAAET
LKATEETFKLSYGIATVREVLSRELHLSWEVGKPRPPLNRNYVFTGYRVTKNSKVQIGE
YTFEKGDYGDVAVYRGTTTYKLVNGDYFVLTSHTVMPLSAPTLVPQEHYVRITGLYPTLN
ISDEFSSNVANYQKVG MQYSTLQGPPTGKSHFAIGLALYPSARIVYTACSHA AVDAL
CEKALKYLPIDKCSRIIPARARVECFDKFKVNSTLEQYVFCTVNALPETTADIVVFDEIS
MATNYDLSV VNARLRAKHVYIGDPAQLPAPRTLTKGTLEPEYFNSVCRLMKTIGPDMF
LGTCCRCPAEIVDVSALVYDNKLKAHKDKSAQC FKM FYKGVITHDVSSAINRPQIGVVR
EFLTRNPAWRKAVFISPYNSQNAVASKILGLPTQTV DSSQGSEYDYVIFTQT TETAHSCN
VNRENVAITRAKIGILCIMS DRDLYDKLQFTSLEIPRRNVATLQAENV TGLFKDCSKIIT
GLHPTQAPTHLSVDIKFKTEGLCVDIPGIPKDMTYRRLISMMGFKMNYQVNGYPNMFITR
EEAIRHVRAWIGFDVEGCHATRDAVG TNLPLQLGFSTGVNLVAVPTGYVD TENNTEFTRV
NAKPPPGDQFKHLIPLMYKGLPWNVVR IKIVQMLS DTLKGLSDRVV FVLWAHGFELTSMK
YFVKIGPERTCCLCDKRATCFSTSSDTYACWNH SVGF DYVYNPFMIDVQQWGFTGNLQSN
HDQHCQVHGNHVASCD AIMTRCLAVHECFVKRVDWSVEYPIIGDELRVNSACR KVQHMV
VKSALLADKFPVLHDIGNPKA IKCVPQAEVEWKFYDAQPCSDKAYKIEELFY SYATHHDK
FTDGVC LFWNCNVDRYPANAIVCRFDTRVLSNLNLP GCDGGS LYVNKHAFHTPAFDKSAF
TNLKQLPFFYYSDSPCESH GKQVVS DIDIYVPLKSATCITRCNLGGAVCRHHANEYRQYLD

AYNMMISAGFSLWIYKQFDTYNLWNTFTRLQSLENVAYNVVNKGHFDGHAGEAPVSIINN
AVYTKVDGIDVEIFENKTTLPVNVAFELWAKRNIKPVEIKILNNLGVDIAANTVIWDYK
REAPAHVSTIGVCTMTDIAKKPTESACSSLTVLFDGRVEGQVDLFRNARNGVLITEGSVK
GLTPSKGPAQASVNGVTLIGESVKTQFNFKKVDGIIQQLPETYFTQSRDLEDFKPRSQM
ETDFLELAMDEFIQRYKLEGYAFEHIVYGDFSHGQLGGLHLMIGLAKRSQDSPLKLEDFI
PMDSTVKNYFITDAQTGSSKCVCSVIDLLDDFVEIISQDLSVISKVVKVTIDYAEISF
MLWCKDGHVETFYPKLQASRAWQPGVAMPNLYKMQRMLLEKCDLQNYGENAVIPKGIMMN
VAKYTQLCQYLNTLTAVPYNMRVIFHGAGSDKGVAPGTAVLRQWLPTGTLLVDSDLNDF
VSDAYSTLIGDCATVHTANKWDLIISDMYDPRTKHVTKENDSKEGFFTYLCGFIKQKLAL
GGSIAVKITEHSWNADLYKLMGHFSWWTAFVTNVNASSSEAFBIGANYLGKPKEQIDGYT
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ENNRVVVSSDILVNN-TNMFIFLLFLTTLTSGSDDLDRCTTFDDVQAPNYTQHTSSMRGVYY
PDEIFRSDTLYLTQDLFLPFYSNVTGFHTINHTFGNPVIFPKDGIYFAATEKSNVVRGW
FGSTMNNKSQSVIIINNSTNVVIRACNFELCDNPFPAVSKPMGTQHTMIFDNAFNCTFE
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PLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYDENGITDAVDCSQNP
LAELKCSVKSFEDKGIYQTSNFRVVPVSGDVVRFPNITNLCPFGEVFNATKFPSPVYAWER
KKISNCVADYSVLNSTFFSTFKCYGVSATKLNLDLCSNVYADS FVVKGD D D V R Q I A P G Q T
GVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNNYKYRYLRHGKLRPFERDISNVPFSP
DGKPCTPPALNCYWPLNDYGFTTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTD LIKN
QCVNFNFNGLTGTGVLTPSSKRFPFQFQGRDVSDFTDSDVRDPKTSEILDISPACFGGVS
VITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHV
DTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSI
SITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTRE
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LGDINARDLICAQKFNGLTVLPLLLTDDMIAAYTAALVSGTATAGWTFGAGAAALQIPFAM
QMAYRFNGIGVTONVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALN
TLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTYQQLIRAAEIRA
SANLAATKMSECVLGQSKRVDFCGKGYHLSFPQAAPHGVVFLHVTYVPSQERNETTAPA
ICHEGKAYFPREGVFVFNGTSWFITQRNFFSPQIITTDNTFVSGNCDVIGIINN TVYDP
LQPELDSFKEELD KYFKNHTSPD VDLGDISGINASV VNIQKEIDRLNEVAKNLNESLIDL
QELGKYEQYIKWPWYVWLGFIAGLIAIVMVTILLCCMTSCCSCCLKGACSCGSCCKFDEDD
SEPV LKG V K L H Y T - T N L W I C L - D F L L L D Q L L H S Q - K L T M L L L Q V L F M L Q Q R Y R Y K P H S L S
D G L L L A L H F L L F F R A L P K - L R S I K D G S - P F I R A S S S F A I Y C C Y L L P S I H I F C L S L Q V W R R
N F C T S M P - Y I F Y N A S T H V E L L - D V G F V G S A N P R T H Y F M M P T T L F A G T H I T M T T V Y H I T V S
Q I Q L S L L K V T A F Q H Q N S K K T T K L V V I L R I G T Q V L K T M S L Y M A I S P K F T T S L S L H K L L Q T L
V L K M L H S S S L T S L L K T H R M C K Y T Q S T A L Q E L L I Q Q W I Q F M M S R R R L L A C L C K H K K V S T N L
C T H S F R K K Q V R - - L I A Y F F F L L S W Y S C - S H - P S L L R F D C V R T A A I L L T - V - - N Q R F T S T R
V L K I - T L L K E F L I F W S K R T N Y Y Y S V W N F N I A Y H G R Q R Y Y Y R - G A - T T P G T M E P S N R F P I
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R L D V A - L L R C F L Q A V C S Y P L N V V I Q P R N K H S S Q C A S P G D N C D Q T A H G K - T C H W C C D H S W S
L A N G R T L P R A L - H - G P A K R D H C G Y I T N A F L L Q I R S V A A C R H - F R E C C I Q P L P Y W K L - I K Y
R P R R - Q R Q Y C F A S T V S D N R C F I L L T S R L Q - Q R Y - L S L - G L S G L L F G I L T L - - V Q - - D N Y L
S L - L R R I I R S - M M K N L W S - I I H K T N M K I I L F L T L I V F T S C E L Y H Y Q E C V R G T T V L L K E P C
P S G T Y E G N S P F H P L A D N K F A L T C T S T H F A F A C A D G T R H T Y Q L R A R S V S P K L F I R Q E E V Q Q
E L Y S P L F L I V A A L V F L I L C F T I K R K T E - M S S L - L T S I C A F - P F C Y S L F - - C L L Y F G F H S K
S R I - K N L V P K S K R T - N F S L F - L V F L Y A V A Y A L - Y S A V H L I N L M C L K I L V R Y N T R G N T Y S T
A W L C A L G K V L P F H R W H T M V Q T C T P N V T I N C Q D P A G G A L I A R C W Y L H E G H Q T A A F R D V L V V
L N K R T N - N V - - W T P I K P T - C P P H Y I W W T H R E N - Q - P E W R T Q W G K A K T A P T P R F T Q - Y C V L
V H S S H A W Q G G T - I P S R P G R S N Q H Q - W S R - P N W L L P K S Y P T S S W W - R Q N E R A Q P Q M V L L L
P R N W P R S F T S L R R - Q R R H R M G C N - G S L E Y T Q R P H W H P Q S - - Q C C H R A T T S S R N N I A K R L L
R R G K Q R R Q S S L F S L L I T - S R - F K K F N S W Q Q - G K F S C S N G - R R W - N C P R A I A A R Q I E P A - E
Q S F W - R P T T T R P N C H - E I C C - G I - K A S P K T Y C H K T V Q R H S S I W E T W S R T N P R K F R G P R P N
Q T R N - L Q T L A A N C T I C S K C L C I L W N V T H W H G S H T F G N M A D L S W S H - I G - Q R S T I Q R Q R H T
A E Q A H - R I Q N I P T N R A - K G Q K E K D - - S S A F A A E T K E A A H C D S S S C G - H G - F L Q T T S K F H E

WSFC-FNSGINTHDDHTRQMGYVNVFAIPFTIHSLLLCRMNSRN-TAQVGLVNFNLT-QS
LINV-H-GGLERATTFSSRPRGVRSRVQ-IMLGRAAYMEEP-CVKLILVVLSPCDFNSFL

FIGURE 25

PTPRTLDAVCGCINVFKRVCVSAARLTPCGTGTSTDVVYRAFDIYNEKVAGFAKFLKTNCCRFQEK
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LVYALRHFDEGNCDTLKEILVTYNCCDDDYFNKKDWYDFVENPDILRVYANLGERVRQSLLKTVQFC
DAMRDAGIVGVLTLDNQDLNGNWDYDFGDFVQVAPGCGVPIVDSYYSLLMPILTLTRALAAESHMDAD
LAKPLIKWDLKDYDFTEERLCLFDRYFKYWDQTYHPNCINCLDDRCILHCANFNVLFSTVFPPTSFG
PLVRKIFVDGVPFVSTGYHFRELGVVHNQDVNLHSSRLSFKELLVYAADPAMHAASGNLLLDKRTT
CFSVAALTNNVAFQTVKPGNFNKFDFYDFAVSKGFFKEGSSVELKHFFFAQDGNAAISDYDYRYNLP
TMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDKSAGFPFNKWGKARLYYDSMSYEDQDALF
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SSQGSEYDYVIFTQTETAHSCNVNRFNVAITRAKIGILCIMSDDRDLYDKLQFTSLEIPRRNVATLQ
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GYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQLGFGSTGVNLVAVPTGYVDTENNTFT
RVNAKPPPGDKFKHLIPLMYKGLPWNVVRKIVQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKI
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VASCDAIMTRCLAVHECFVKRVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNP
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VNKGHFDGHAGEAPVSIINNAVYTKVDGIDVEIFENKTTLPVNVAFELWAKRNIKPVPEIKILNNLG
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SSSEAFILIGANYLGKPKQIDGYTMHANYIFWRNTNPIQLSSYSLFDMSKFPLKLRGTAVMSLKENQ
INDMIYSLLEKGRLIIRENNRVVVSSDILVNN*TNMFIFLLFLTSTSGSDLDRCTTFDDVQAPNYTQ
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GWVFGSTMNNKSQSVIIINNSTNVVIRACNFELCDNPFFAVSKPMGTQTHMIFDNAFNCTFEYISD
AFSLDVSEKSGNFKHLREFVFNKDGFLYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINITNFRA
ILTAFSPAQDIWGTSAAYFVGYLKPTTFMLKYDENGITITDAVDCSQNPLAELKCSVKSFEIDKGIY
QTSNFRVVPBGDVVRFPNITNLCPFGEVFNATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCY
GVSATKLNLDLCSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPPDDFMGCVLAWNTRNIDATSTG
NINYKYRYLRHGKLRPFERDISNVPFSPDGKPCPPALNCYWPLNDYGFYTTTGIGYQPYRVVVLSE
ELLNAPATVCGPKLSTDLIKNCVNFNFNGLTGTGVLTSSSKRFQPFQFGRDVSDFDTSVRDPKTS
EILDISPCAFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTAWRIYSTGNNVFQTQAGC
LIGAEHVDTSYECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSI

SITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQ
 MYKTPTLKYFGGFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQK
 FNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQK
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 AEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQA
 APHGTVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVVFVNGTSWFITQRNFFSPQIITTDNTFV
 SGNCDDVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEV
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 DEDDSEPV LKGVKLHYT*

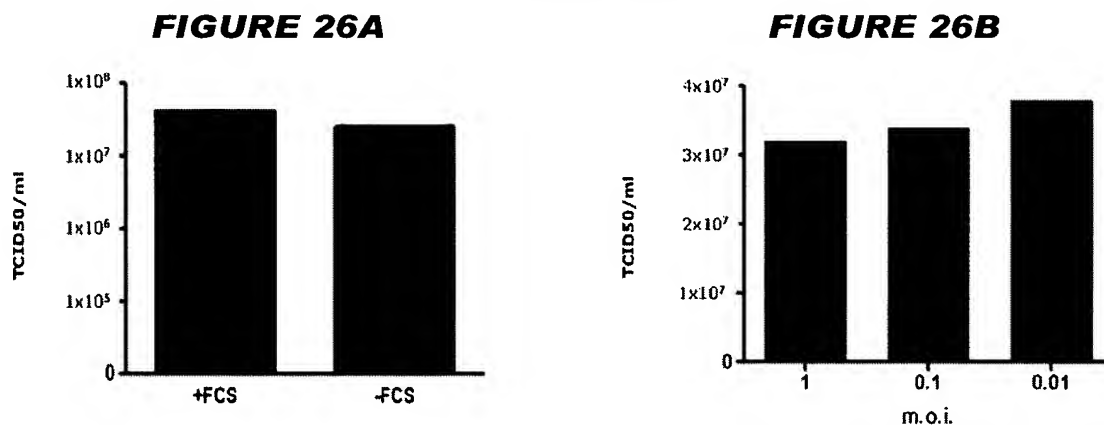
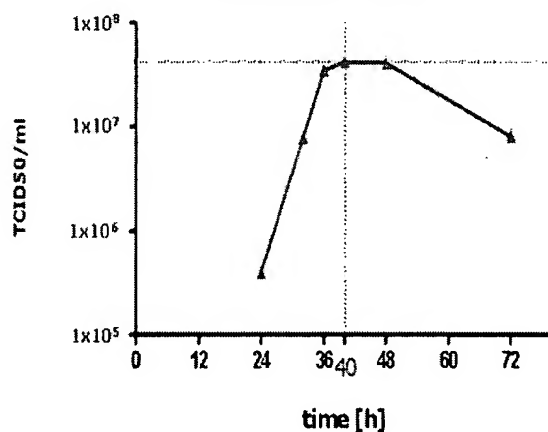
FIGURE 26**FIGURE 26C**

FIGURE 27

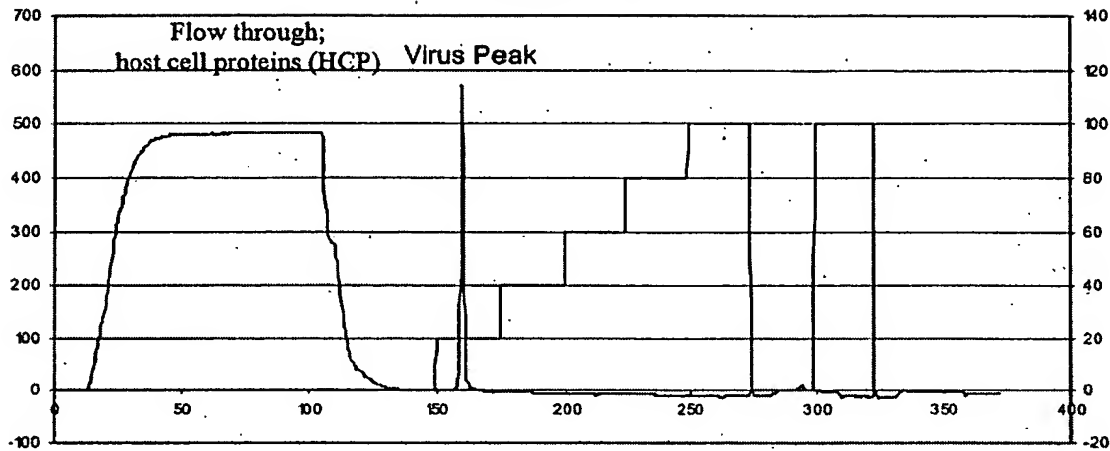
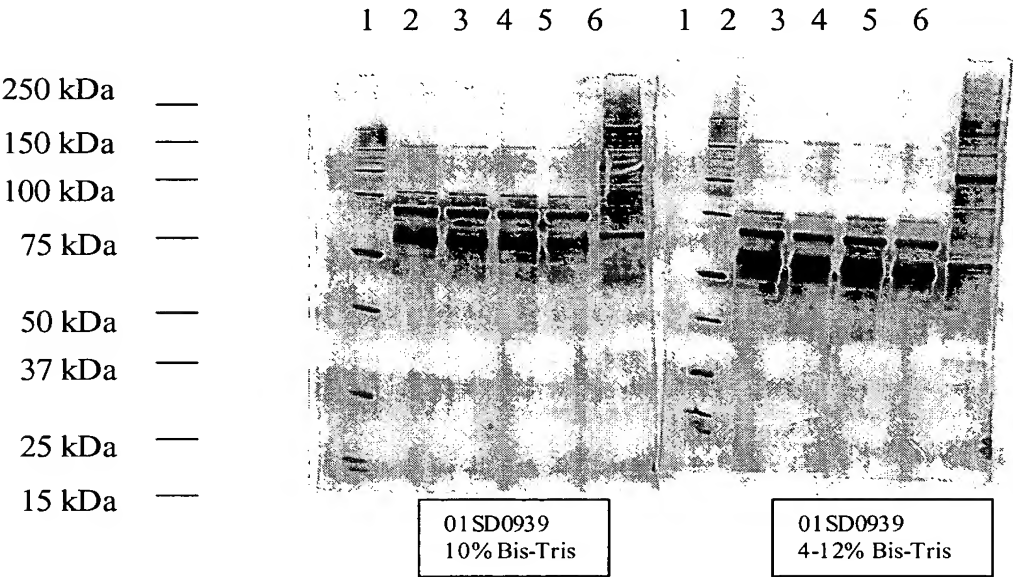
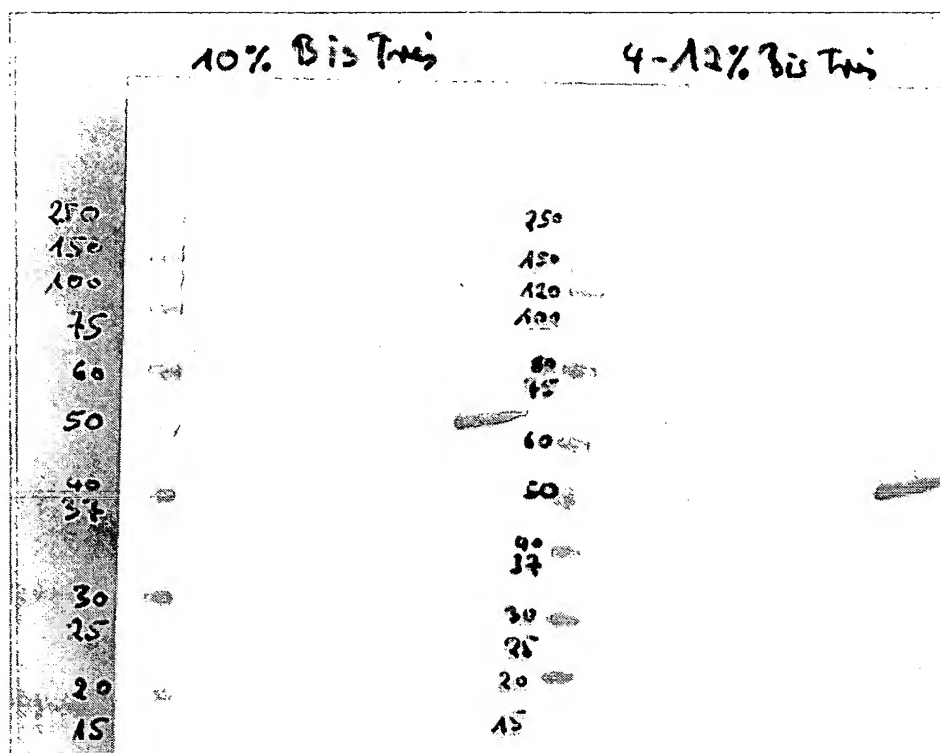
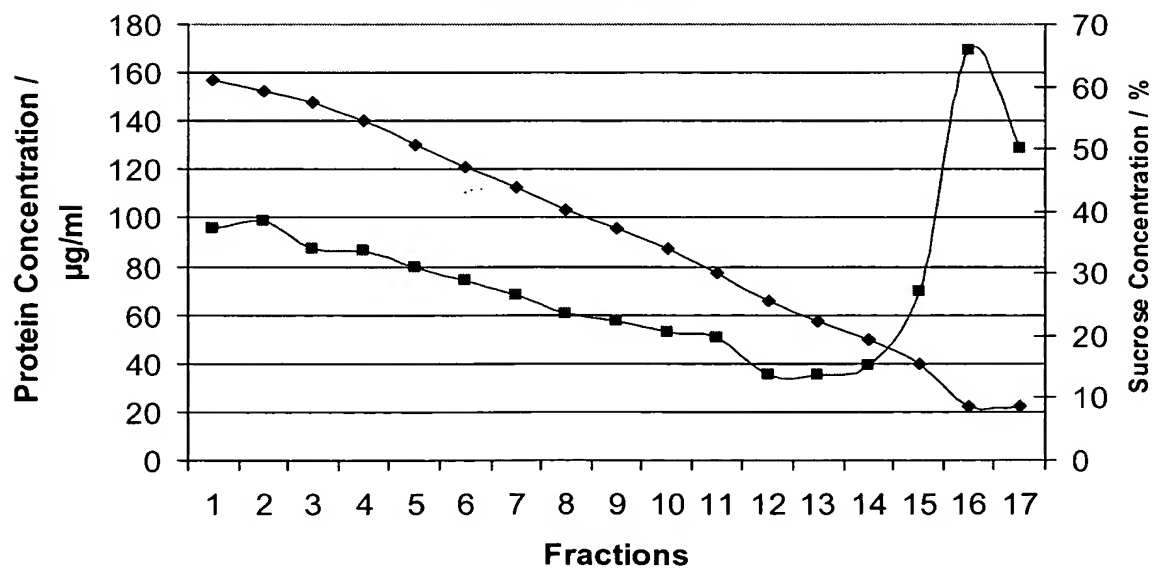


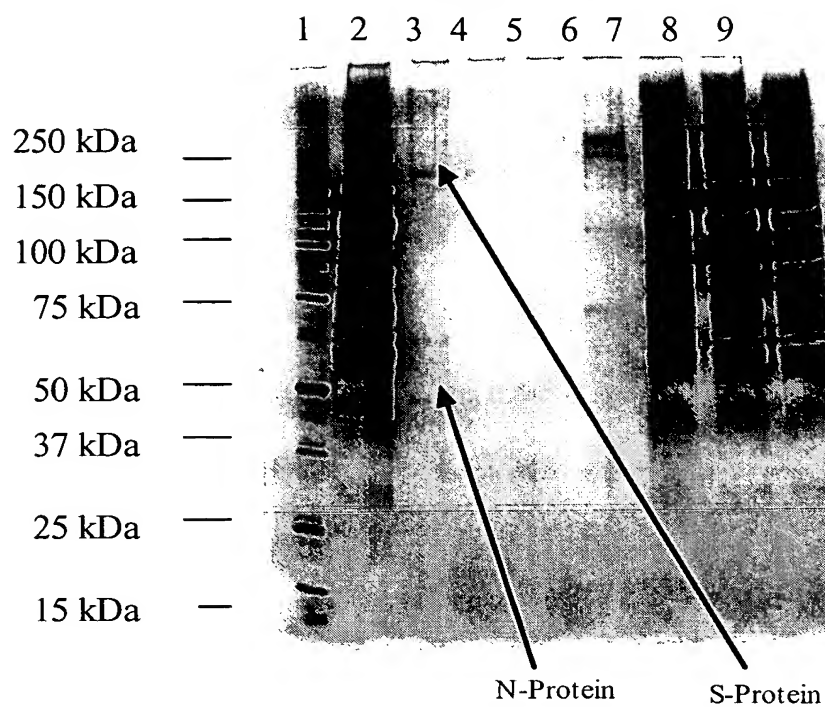
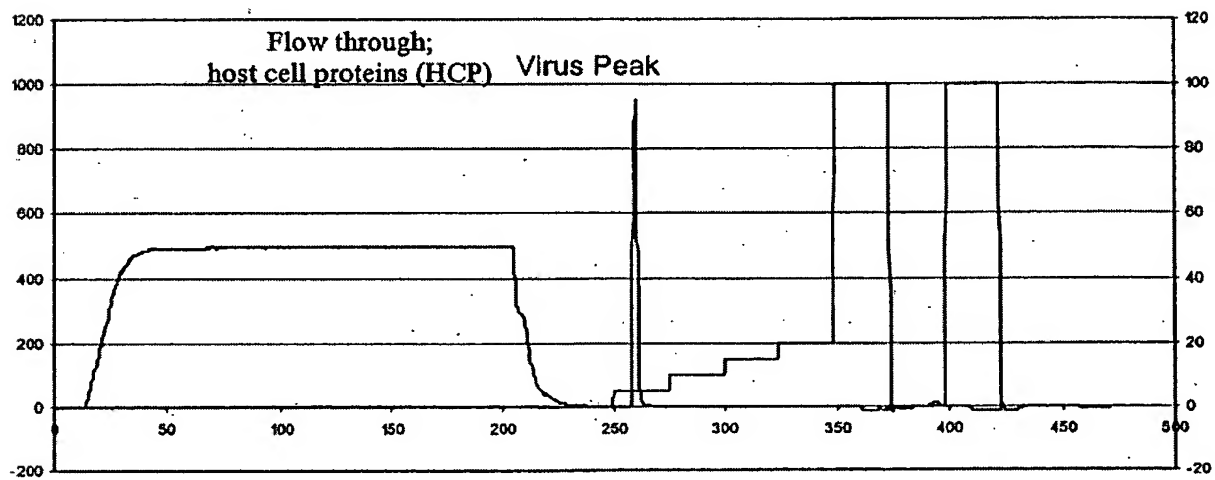
FIGURE 28



94/199

FIGURE 29**FIGURE 30**

95/199

FIGURE 31**FIGURE 32**

96/199

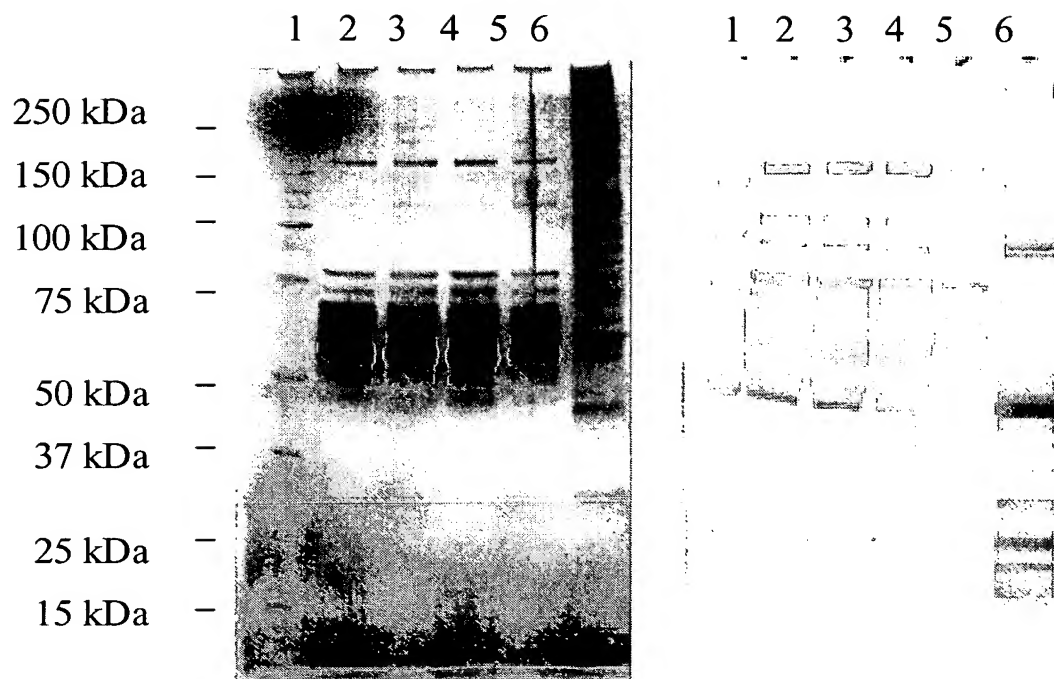
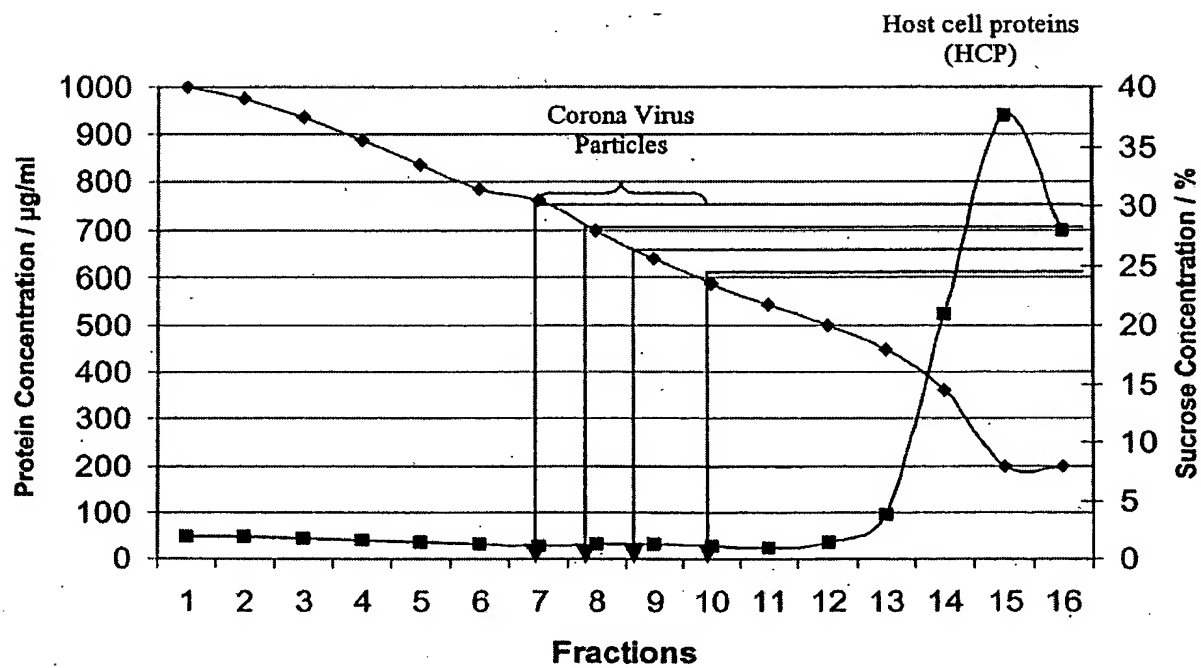
FIGURE 33**FIGURE 34**

FIGURE 35

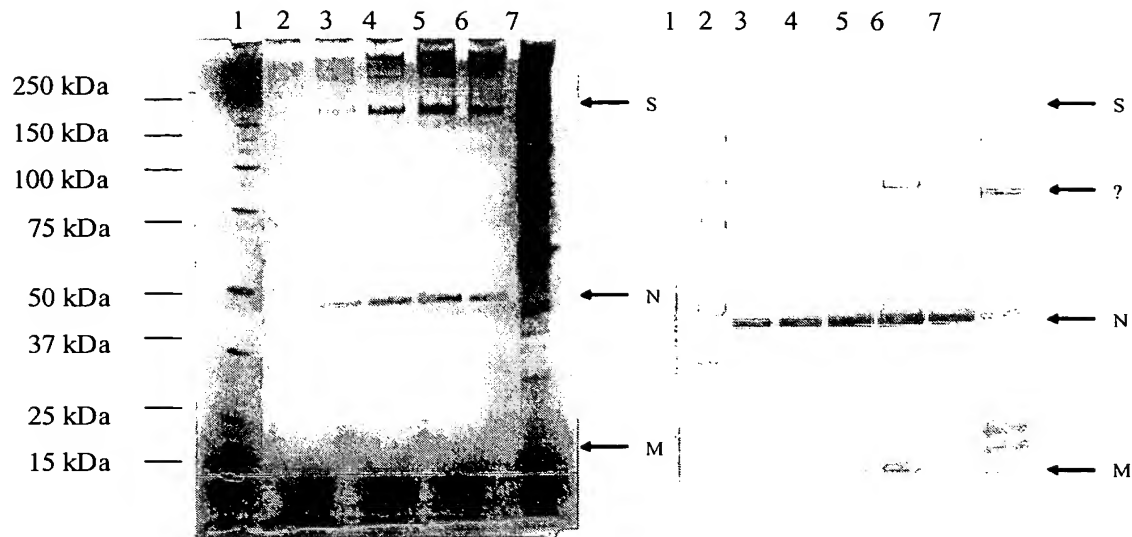


FIGURE 36

FIGURE 36A

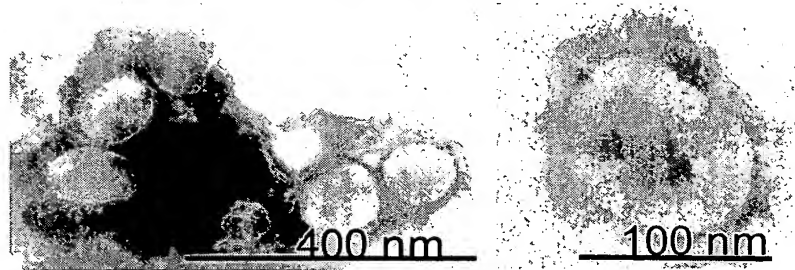


FIGURE 36B

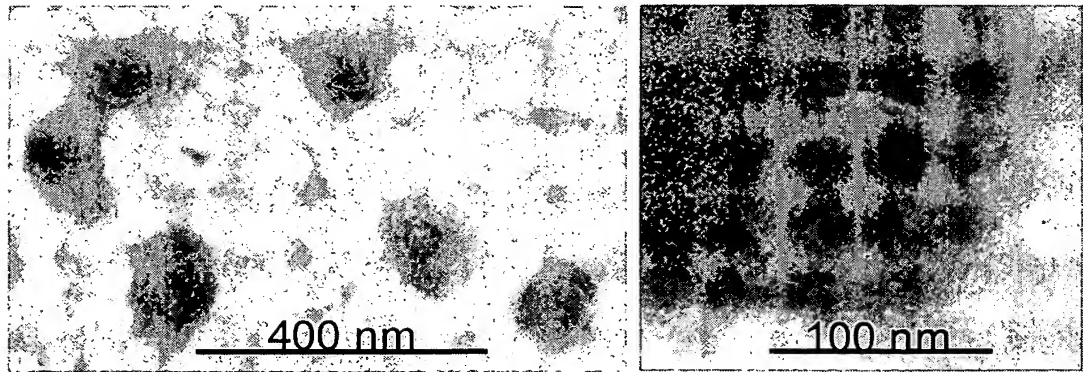
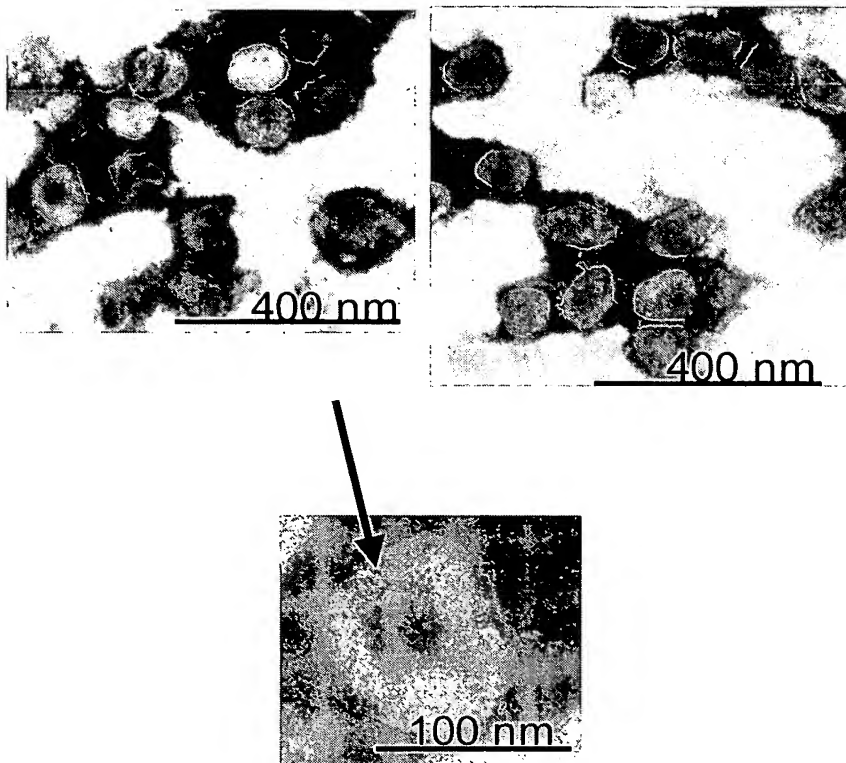


FIGURE 36C



99/199

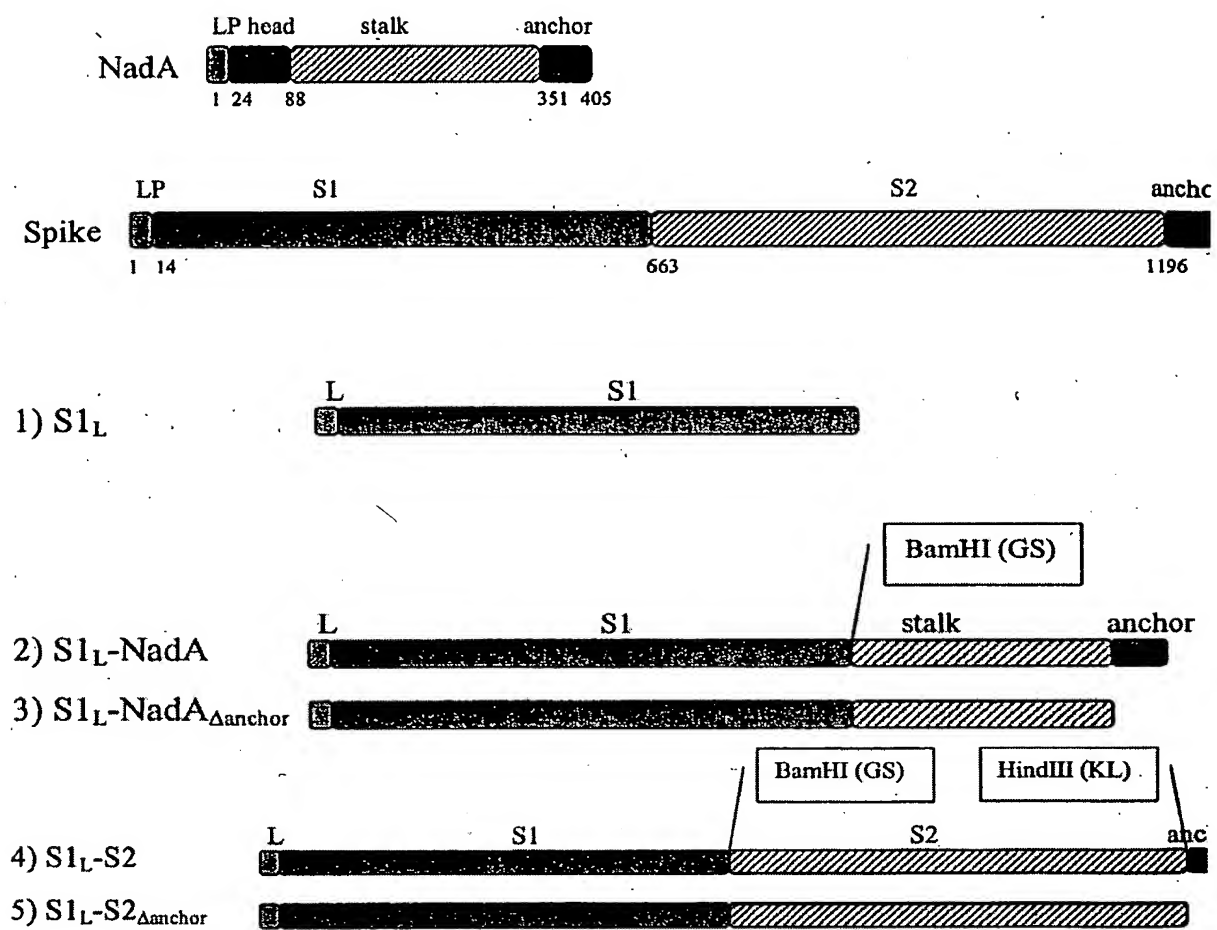
FIGURE 37

FIGURE 38

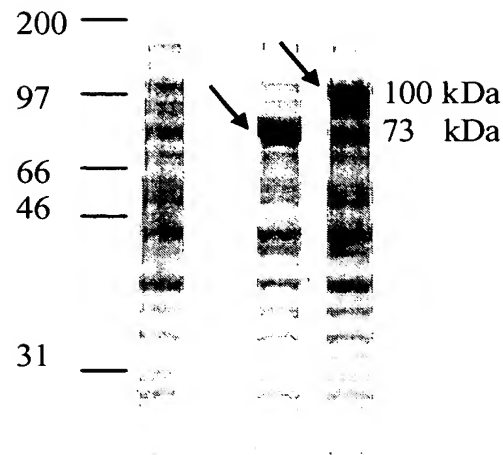


FIGURE 39

FIGURE 39A

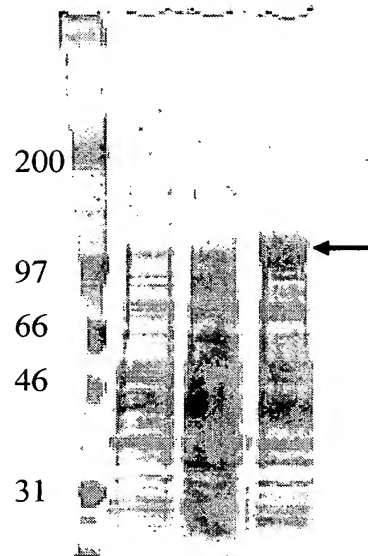


FIGURE 39B

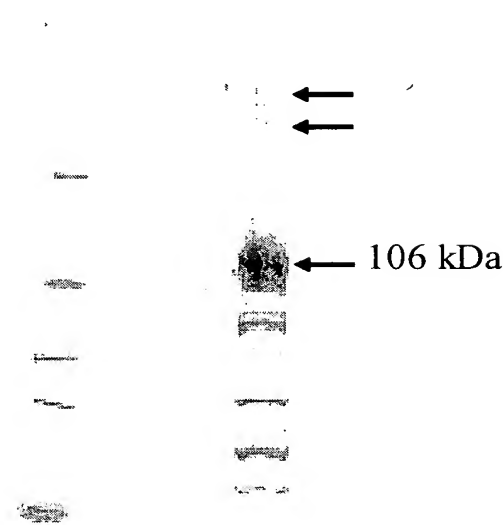


FIGURE 40

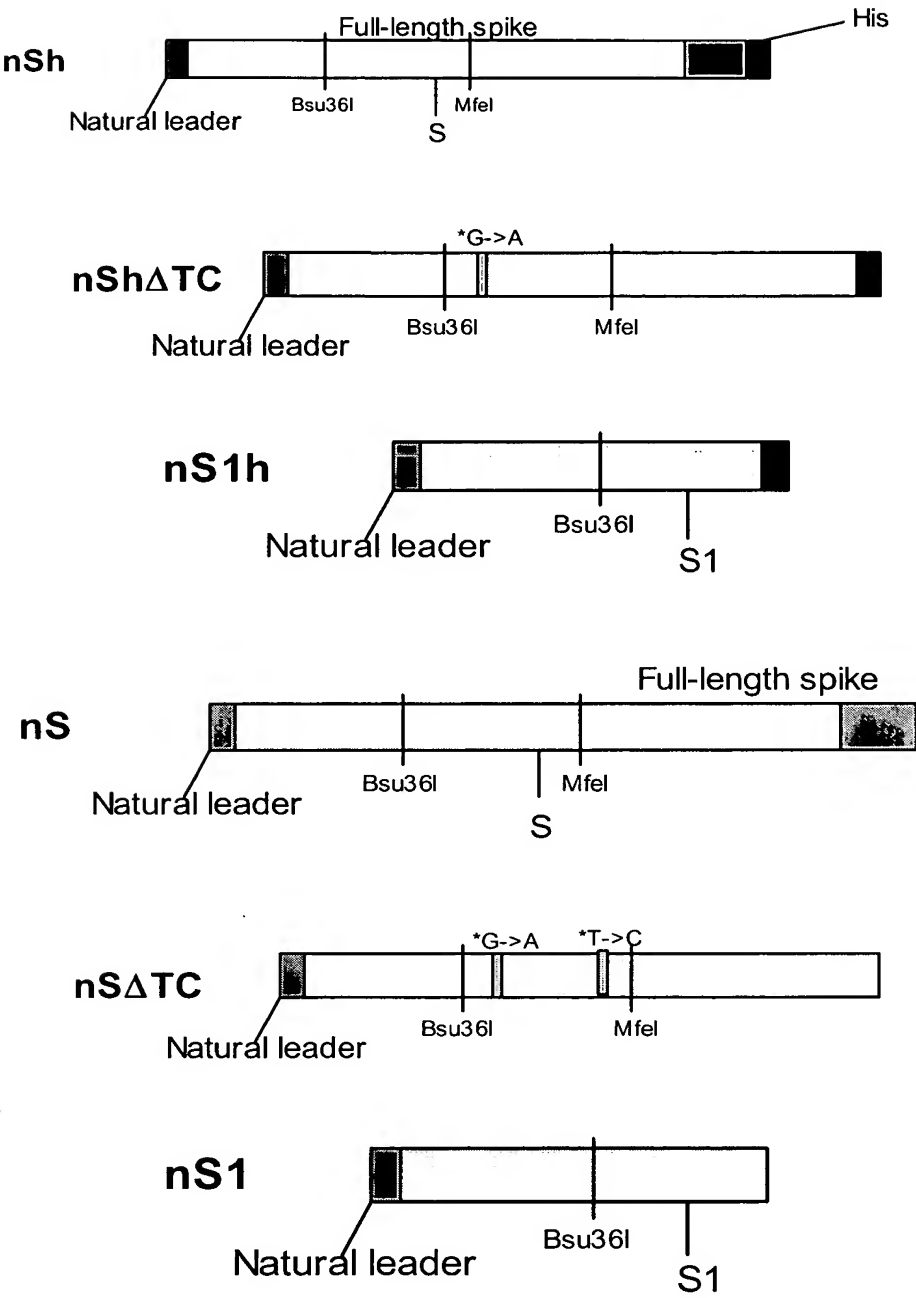


FIGURE 43

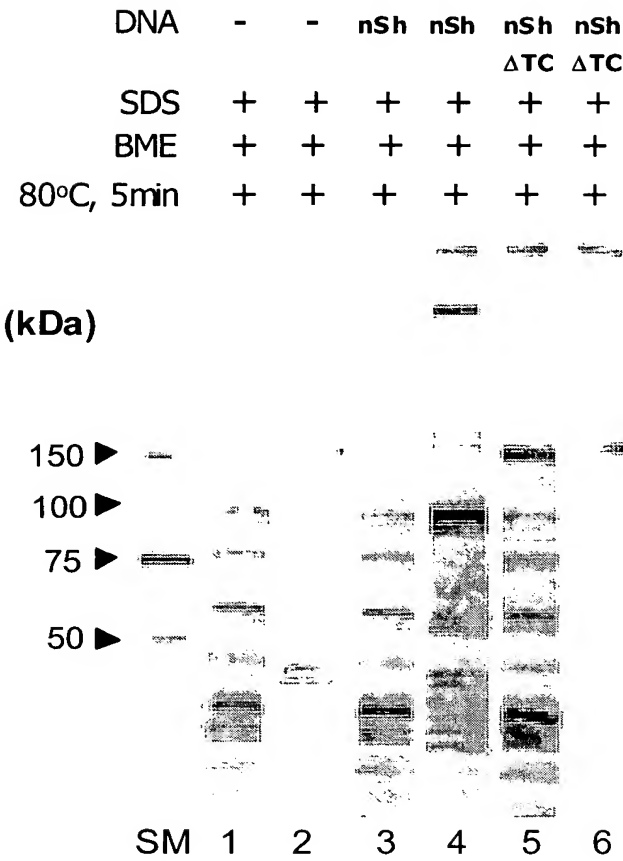


FIGURE 44

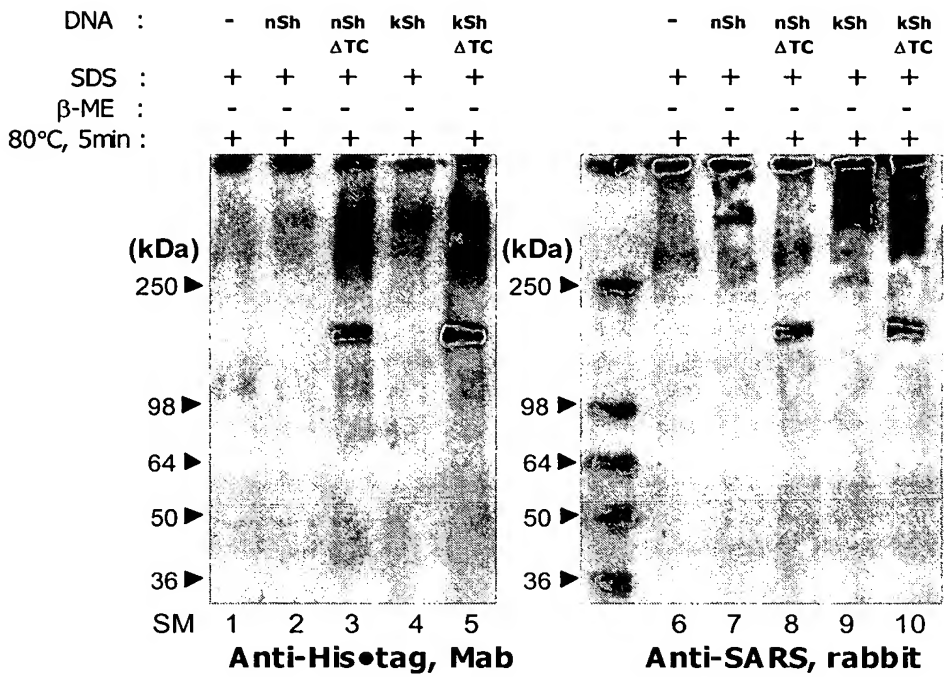


FIGURE 45

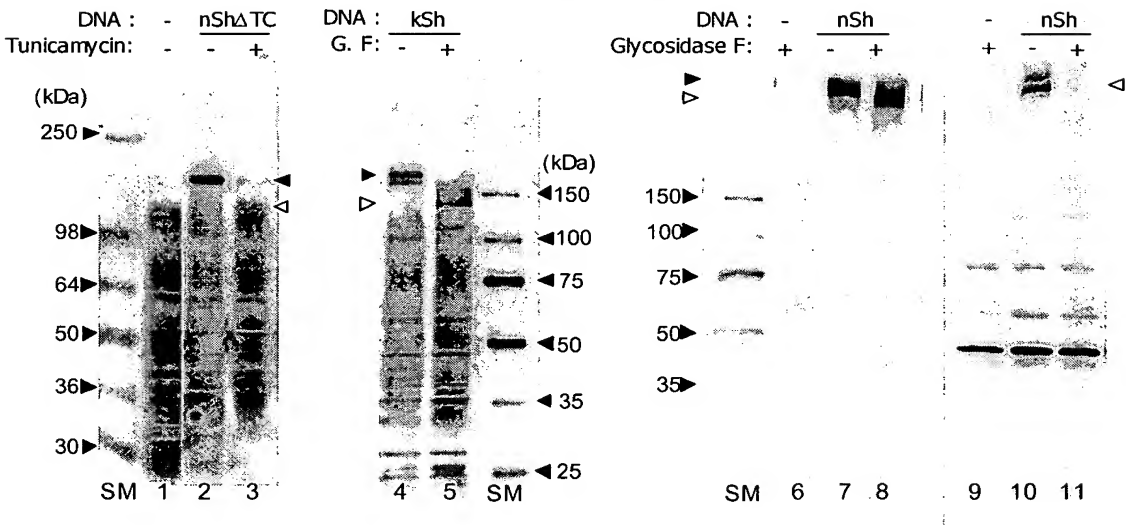


FIGURE 46

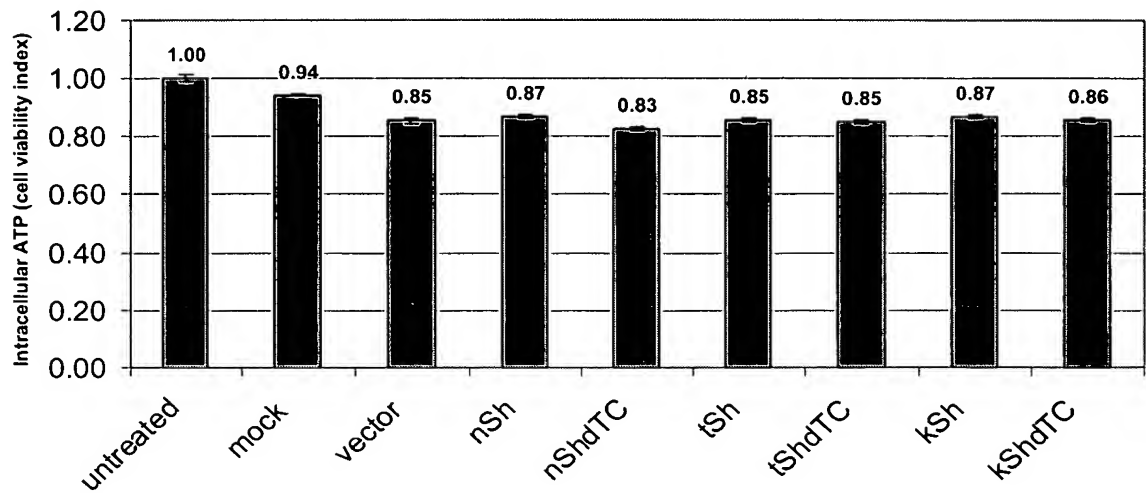


FIGURE 47

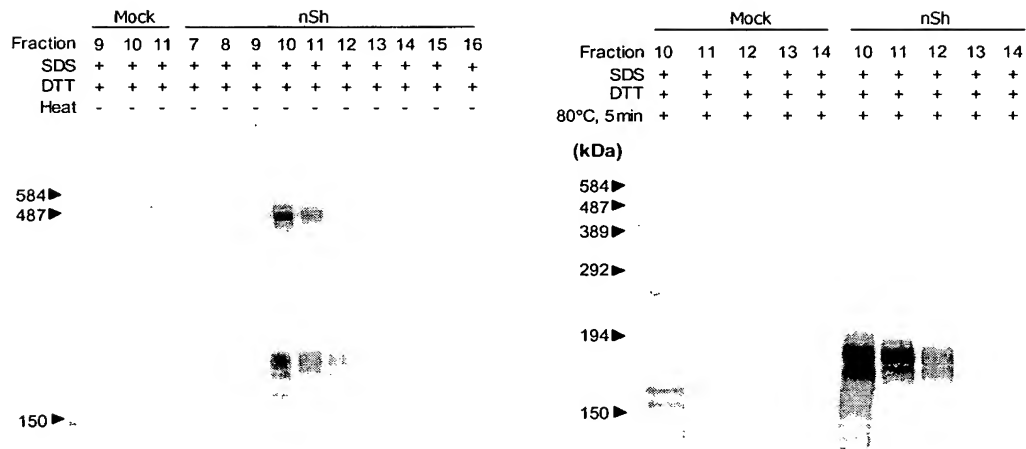


FIGURE 48

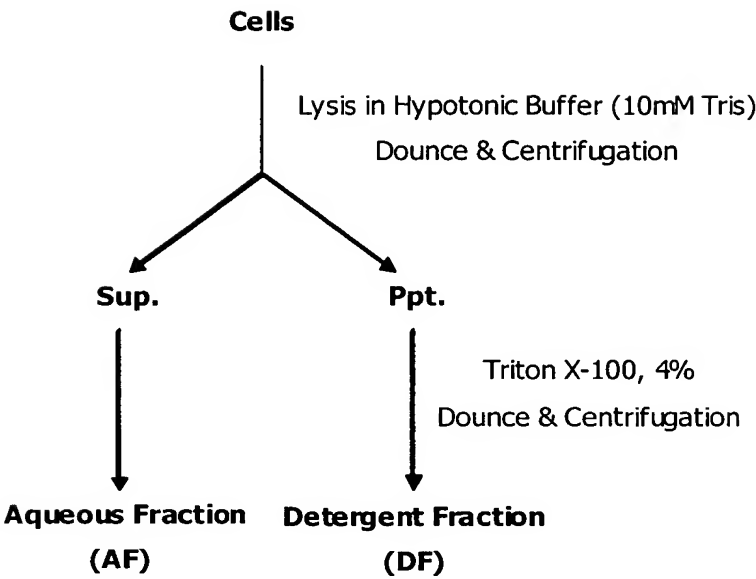


FIGURE 49

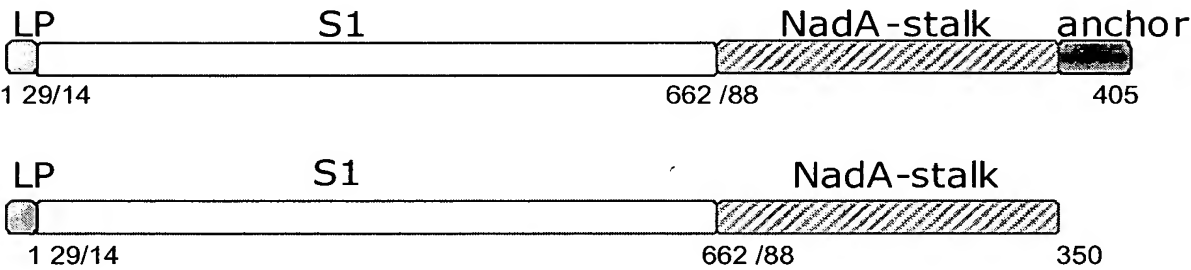
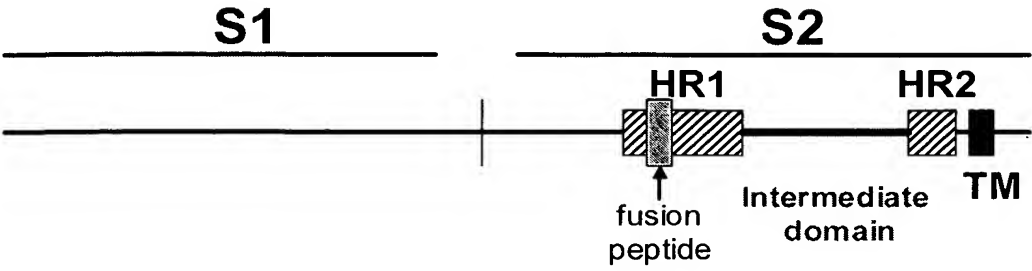


FIGURE 50



- a) Leader(NadA)-HR1-GGGGGG-HR2-GGGGSG-stalk(NadA)-anchor(NadA)
- b) Leader(NadA)-HR1-GGGGGG-HR2-GGGGSG-stalk(NadA)
- c) Leader(NadA)-HR1-intermediate-domain-HR2-GGGGSG-stalk(NadA)-anchor(NadA)
- d) Leader(NadA)-HR1-intermediate-domain-HR2- GGGGSG-stalk(NadA)
- e) HR1-intermediate-domain-HR2- GGGGSG-stalk(NadA) - HHHHHH
- f) Leader(NadA)-HR1-intermediate-domain-HR2-anchor(NadA)
- g) Leader(NadA)-HR1-intermediate-domain-HR2

FIGURE 51

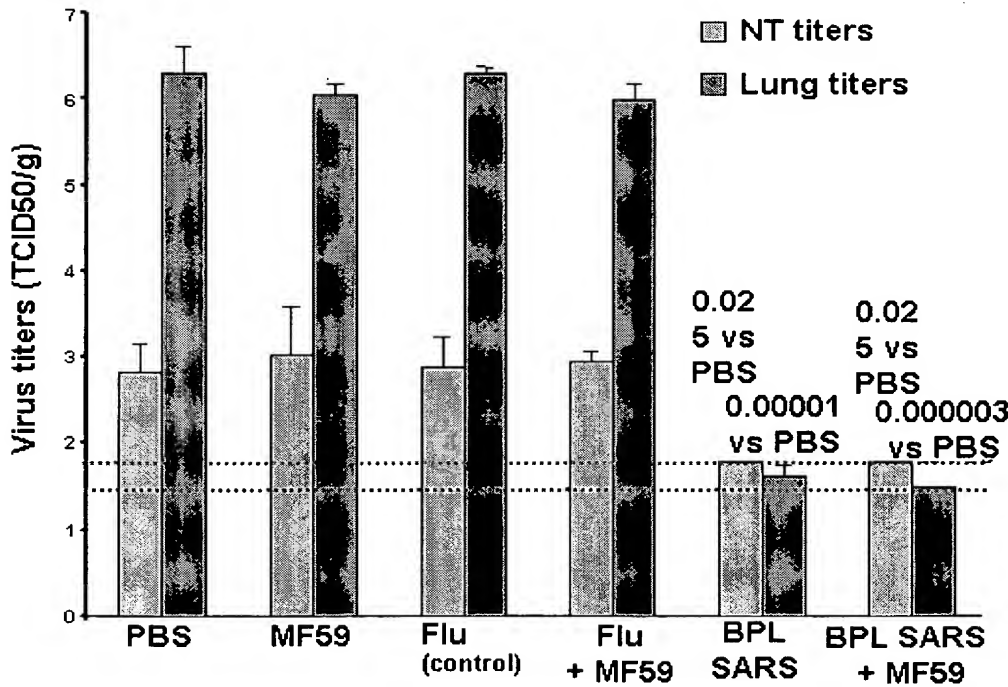
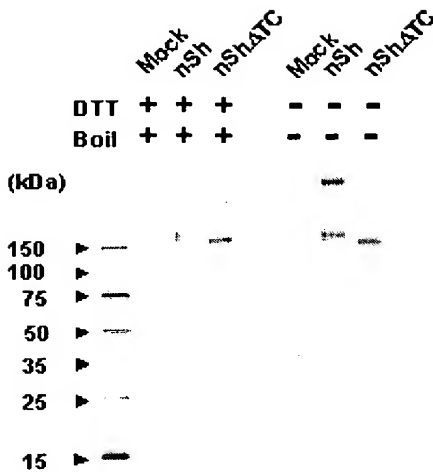


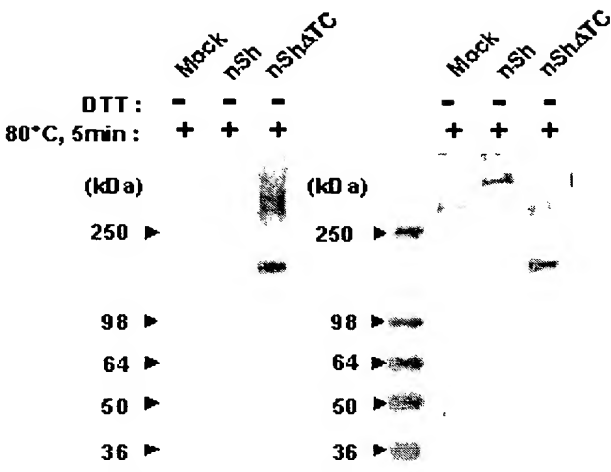
FIGURE 52

A. 293 cell lysates



Anti-His - tag, mAb
4-20% TG SDS gel

B. COS7 cell culture supernatants



Anti-His - tag, mAb Anti-SARS, rabbit
4-20% TG SDS gel

FIGURE 53

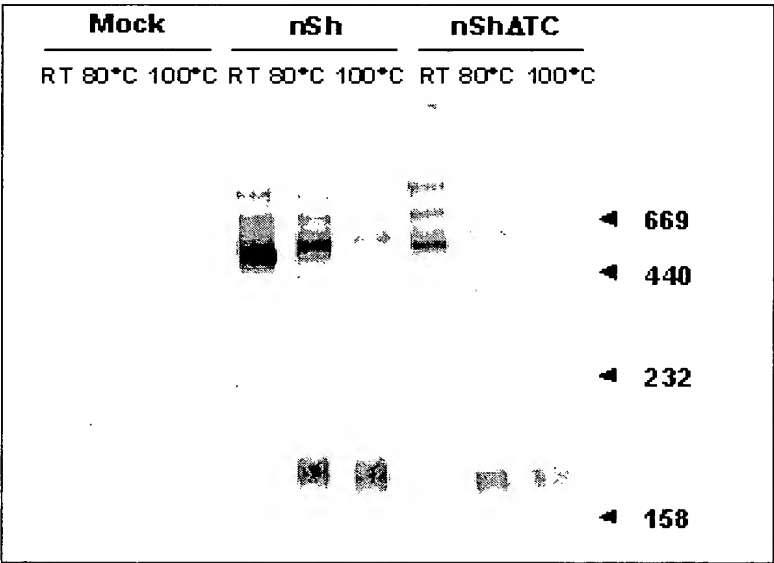


FIGURE 55

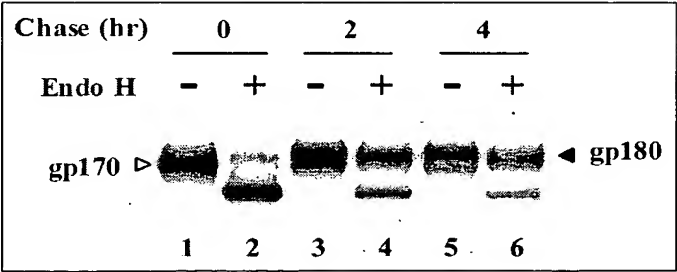


FIGURE 54

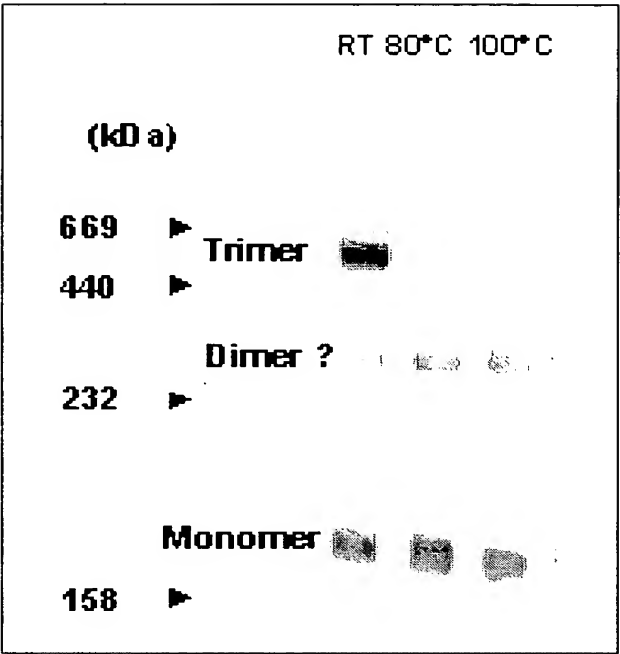


FIGURE 56

FIGURE 56A

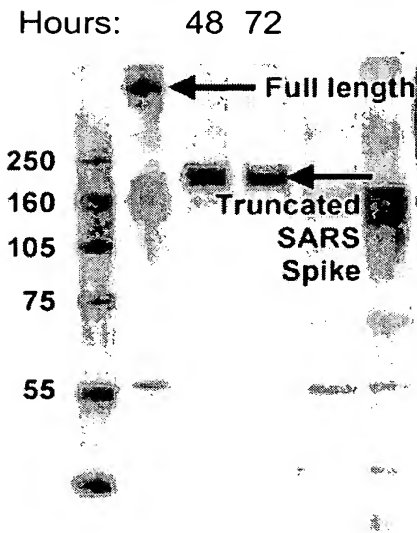


FIGURE 56B

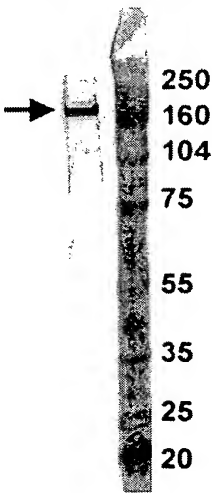
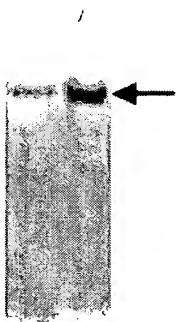
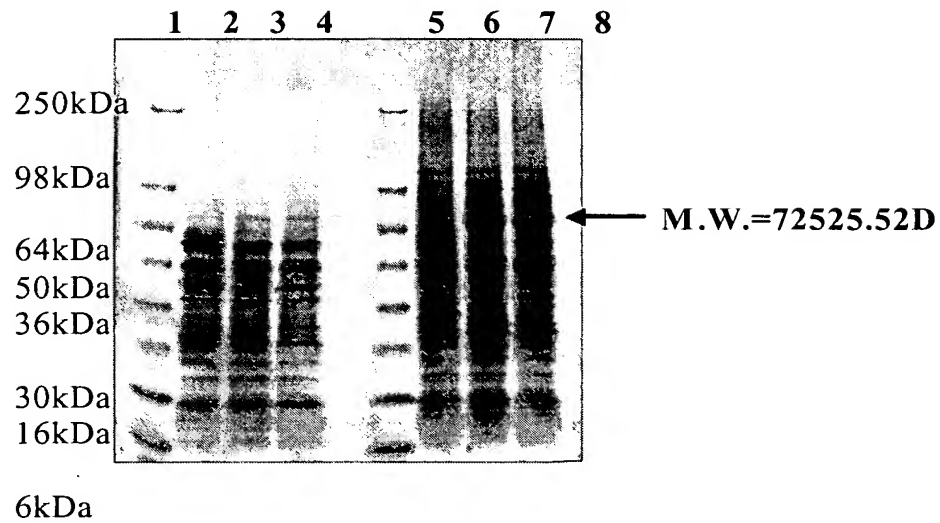
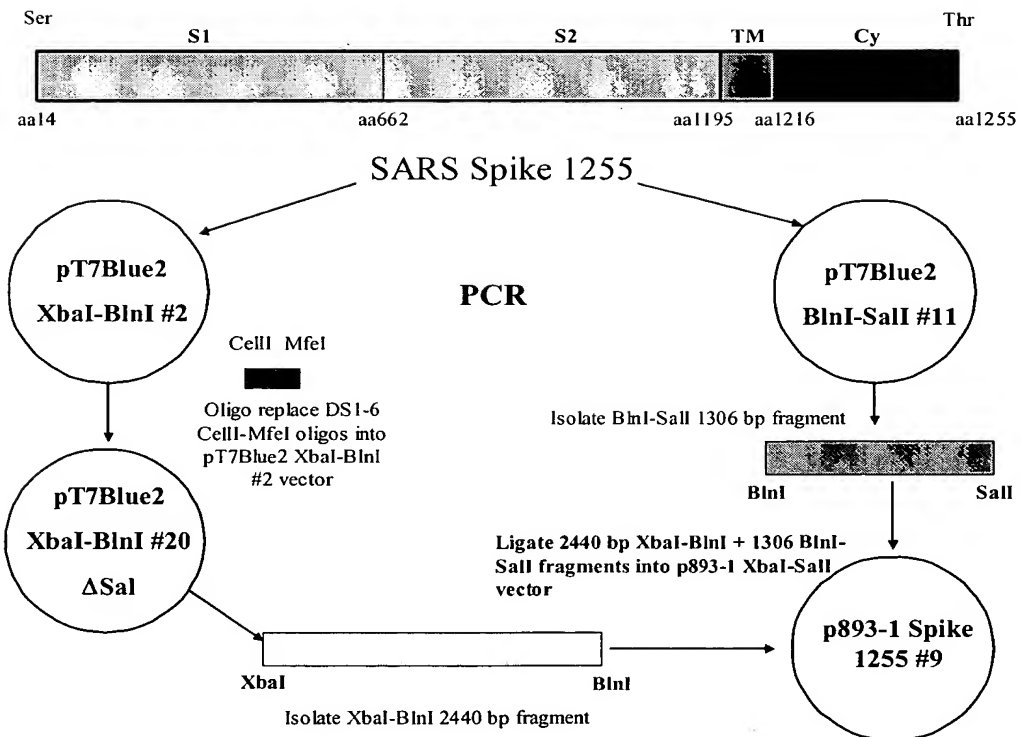


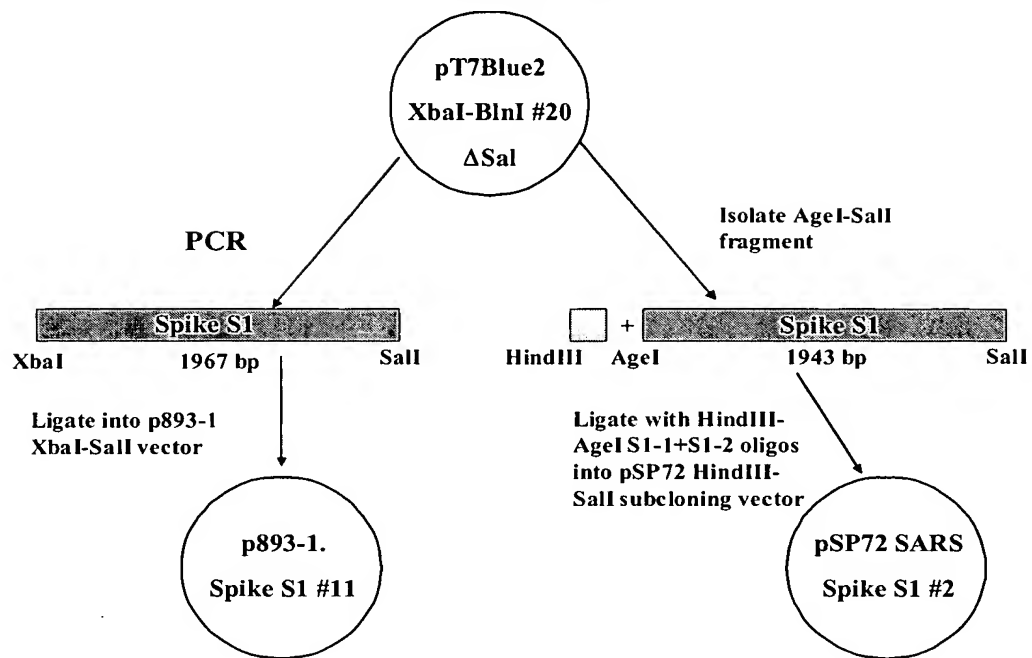
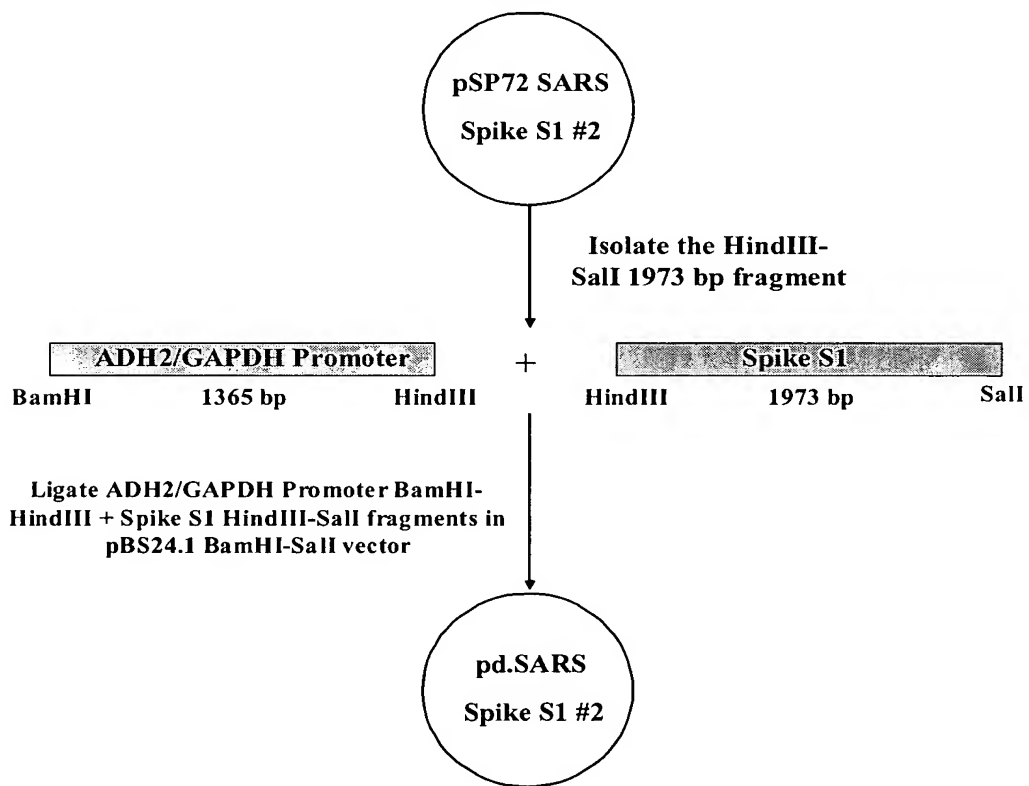
FIGURE 56C



110/199

FIGURE 57**FIGURE 58**

111/199

FIGURE 59**FIGURE 60**

112/199

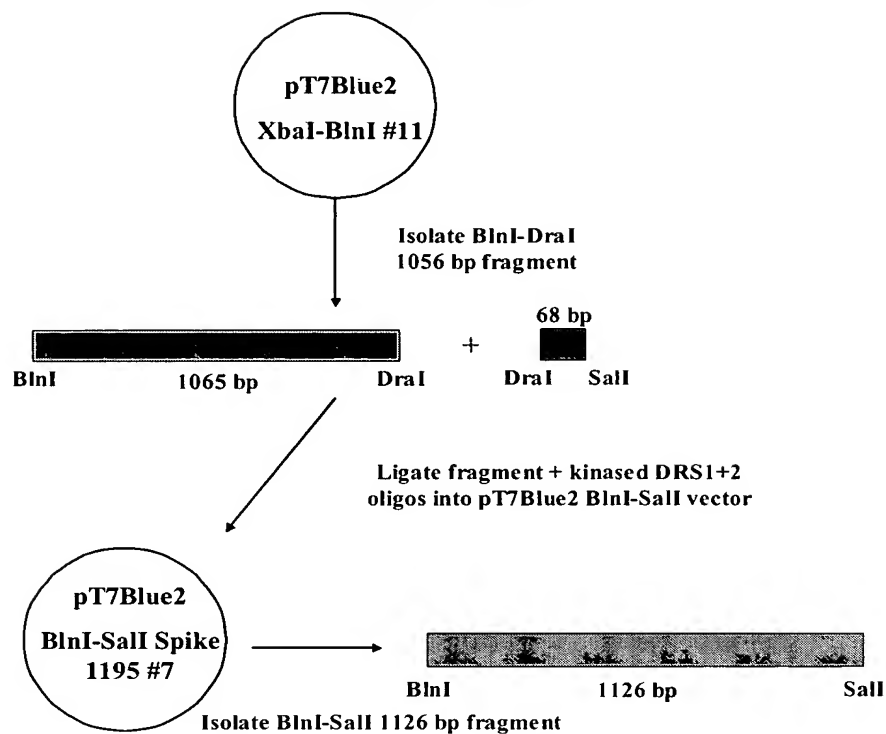
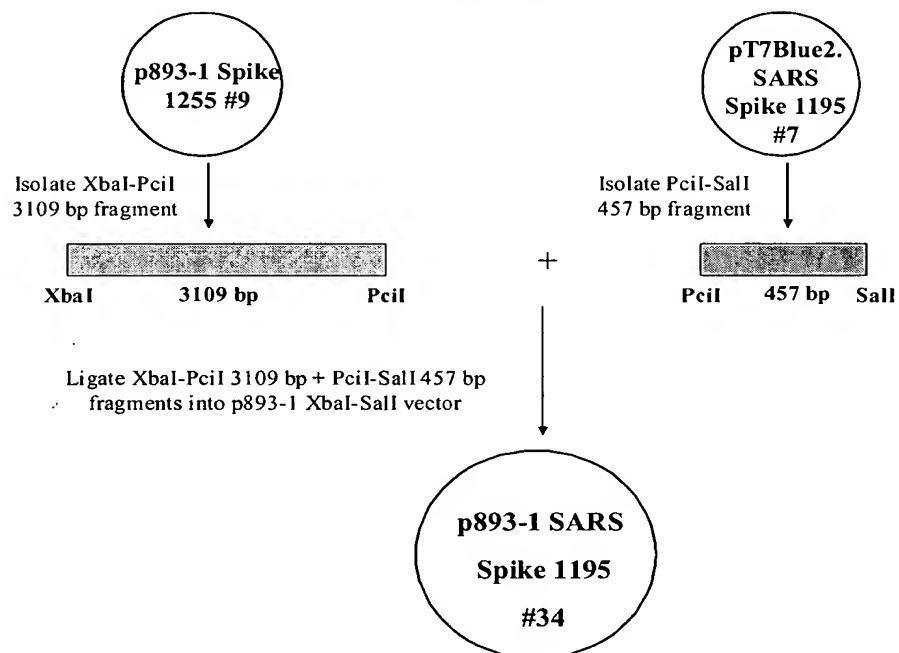
FIGURE 61**FIGURE 62**

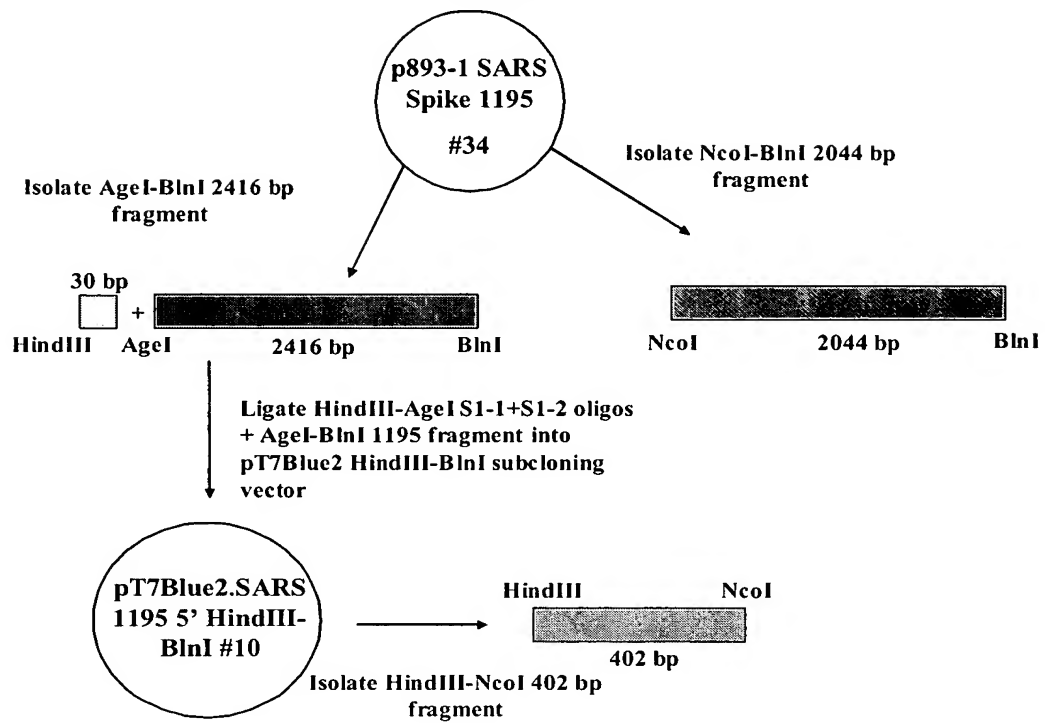
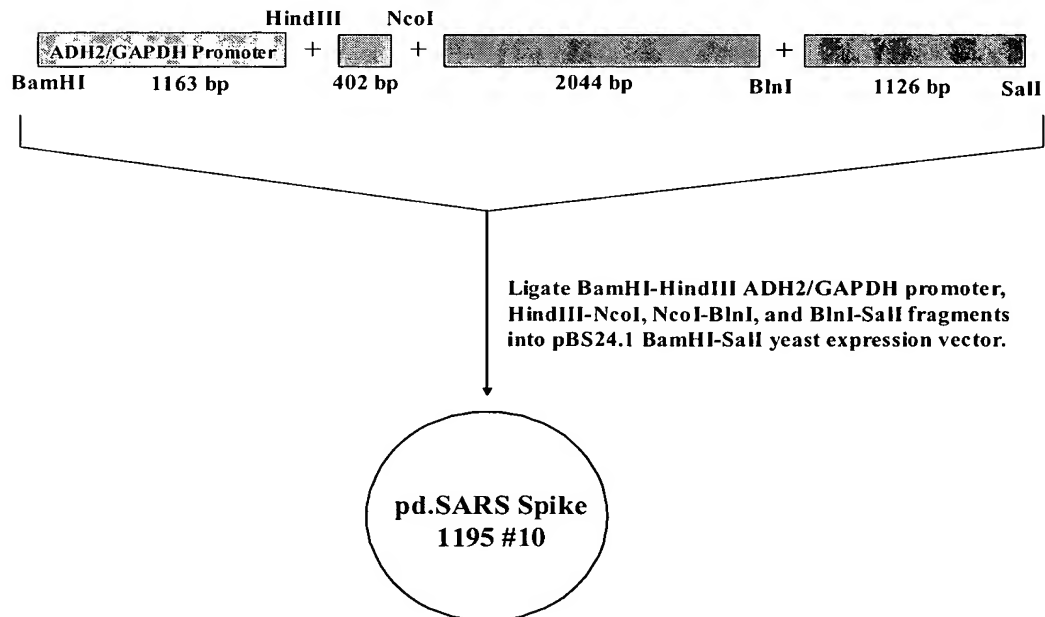
FIGURE 63**FIGURE 64**

FIGURE 65

					1										10
AAGCTTACAAAACAAA					M	S	D	L	D	R	C	T	T	F	
					ATG	AGT	GAC	CTT	GAC	CGG	TGC	ACC	ACT	TTT	
					20										
D	D	V	Q	A	P	N	Y	T	Q	H	T	S	S	M	
GAT	GAT	GTT	CAA	GCT	CCT	AAT	TAC	ACT	CAA	CAT	ACT	TCA	TCT	ATG	
					30										40
R	G	V	Y	Y	P	D	E	I	F	R	S	D	T	L	
AGG	GGG	GTT	TAC	TAT	CCT	GAT	GAA	ATT	TTT	AGA	TCA	GAC	ACT	CTT	
					50										
Y	L	T	Q	D	L	F	L	P	F	Y	S	N	V	T	
TAT	TTA	ACT	CAG	GAT	TTA	TTT	CTT	CCA	TTT	TAT	TCT	AAT	GTT	ACA	
					60										70
G	F	H	T	I	N	H	T	F	G	N	P	V	I	P	
GGG	TTT	CAT	ACT	ATT	AAT	CAT	ACG	TTT	GGC	AAC	CCT	GTC	ATA	CCT	
					80										
F	K	D	G	I	Y	F	A	A	T	E	K	S	N	V	
TTT	AAG	GAT	GGT	ATT	TAT	TTT	GCT	GCC	ACA	GAG	AAA	TCA	AAT	GTT	
					90										100
V	R	G	W	V	F	G	S	T	M	N	N	K	S	Q	
GTC	CGT	GGT	TGG	GTT	TTT	GGT	TCT	ACC	ATG	AAC	AAC	AAG	TCA	CAG	
					110										
S	V	I	I	I	N	N	S	T	N	V	V	I	R	A	
TCG	GTG	ATT	ATT	ATT	AAC	AAT	TCT	ACT	AAT	GTT	GTT	ATA	CGA	GCA	
					120										130
C	N	F	E	L	C	D	N	P	F	F	A	V	S	K	
TGT	AAC	TTT	GAA	TTG	TGT	GAC	AAC	CCT	TTC	TTT	GCT	GTT	TCT	AAA	
					140										
P	M	G	T	Q	T	H	T	M	I	F	D	N	A	F	
CCC	ATG	GGT	ACA	CAG	ACA	CAT	ACT	ATG	ATA	TTC	GAT	AAT	GCA	TTT	
					150										160
N	C	T	F	E	Y	I	S	D	A	F	S	L	D	V	
AAT	TGC	ACT	TTC	GAG	TAC	ATA	TCT	GAT	GCC	TTT	TCG	CTT	GAT	GTT	
					170										
S	E	K	S	G	N	F	K	H	L	R	E	F	V	F	
TCA	GAA	AAG	TCA	GGT	AAT	TTT	AAA	CAC	TTA	CGA	GAG	TTT	GTG	TTT	
					180										190
K	N	K	D	G	F	L	Y	V	Y	K	G	Y	Q	P	
AAA	AAT	AAA	GAT	GGG	TTT	CTC	TAT	GTT	TAT	AAG	GGC	TAT	CAA	CCT	

```

                200
  I   D   V   V   R   D   L   P   S   G   F   N   T   L   K
ATA GAT GTA GTT CGT GAT CTA CCT TCT GGT TTT AAC ACT TTG AAA

                210
  P   I   F   K   L   P   L   G   I   N   I   T   N   F   R
CCT ATT TTT AAG TTG CCT CTT GGT ATT AAC ATT ACA AAT TTT AGA

                230
  A   I   L   T   A   F   S   P   A   Q   D   I   W   G   T
GCC ATT CTT ACA GCC TTT TCA CCT GCT CAA GAC ATT TGG GGC ACG

                240
  S   A   A   A   Y   F   V   G   Y   L   K   P   T   T   F
TCA GCT GCA GCC TAT TTT GTT GGC TAT TTA AAG CCA ACT ACA TTT

                260
  M   L   K   Y   D   E   N   G   T   I   T   D   A   V   D
ATG CTC AAG TAT GAT GAA AAT GGT ACA ATC ACA GAT GCT GTT GAT

                270
  C   S   Q   N   P   L   A   E   L   K   C   S   V   K   S
TGT TCT CAA AAT CCA CTT GCT GAA CTC AAA TGC TCT GTT AAG AGC

                290
  F   E   I   D   K   G   I   Y   Q   T   S   N   F   R   V
TTT GAG ATT GAC AAA GGA ATT TAC CAG ACC TCT AAT TTC AGG GTT

                300
  V   P   S   G   D   V   V   R   F   P   N   I   T   N   L
GTT CCC TCA GGA GAT GTT GTG AGA TTC CCT AAT ATT ACA AAC TTG

                320
  C   P   F   G   E   V   F   N   A   T   K   F   P   S   V
TGT CCT TTT GGA GAG GTT TTT AAT GCT ACT AAA TTC CCT TCT GTC

                330
  Y   A   W   E   R   K   K   I   S   N   C   V   A   D   Y
TAT GCA TGG GAG AGA AAA AAA ATT TCT AAT TGT GTT GCT GAT TAC

                350
  S   V   L   Y   N   S   T   F   F   S   T   F   K   C   Y
TCT GTG CTC TAC AAC TCA ACA TTT TTT TCA ACC TTT AAG TGC TAT

                360
  G   V   S   A   T   K   L   N   D   L   C   F   S   N   V
GGC GTT TCT GCC ACT AAG TTG AAT GAT CTT TGC TTC TCC AAT GTC

                380
  Y   A   D   S   F   V   V   K   G   D   D   V   R   Q   I
TAT GCA GAT TCT TTT GTA GTC AAG GGA GAT GAT GTA AGA CAA ATA

                390
  A   P   G   Q   T   G   V   I   A   D   Y   N   Y   K   L
GCG CCA GGG CAA ACT GGT GTT ATT GCT GAT TAT AAT TAT AAA TTG

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                                410
    P   D   D   F   M   G   C   V   L   A   W   N   T   R   N
CCA GAT GAT TTC ATG GGT TGT GTC CTT GCT TGG AAT ACT AGG AAC

                                420
    I   D   A   T   S   T   G   N   Y   N   Y   K   Y   R   Y
ATT GAT GCT ACT TCA ACT GGT AAT TAT AAT TAT AAA TAT AGG TAT

                                440
    L   R   H   G   K   L   R   P   F   E   R   D   I   S   N
CTT AGA CAT GGC AAG CTT AGG CCC TTT GAG AGA GAC ATA TCT AAT

                                450
    V   P   F   S   P   D   G   K   P   C   T   P   P   A   L
GTG CCT TTC TCC CCT GAT GGC AAA CCT TGC ACC CCA CCT GCT CTT

                                470
    N   C   Y   W   P   L   N   D   Y   G   F   Y   T   T   T
AAT TGT TAT TGG CCA TTA AAT GAT TAT GGT TTT TAC ACC ACT ACT

                                480
    G   I   G   Y   Q   P   Y   R   V   V   V   L   S   F   E
GGC ATT GGC TAC CAA CCT TAC AGA GTT GTA GTA CTT TCT TTT GAA

                                500
    L   L   N   A   P   A   T   V   C   G   P   K   L   S   T
CTT TTA AAT GCA CCG GCC ACG GTT TGT GGA CCA AAA TTA TCC ACT

                                510
    D   L   I   K   N   Q   C   V   N   F   N   F   N   G   L
GAC CTT ATT AAG AAC CAG TGT GTC AAT TTT AAT TTT AAT GGA CTC

                                530
    T   G   T   G   V   L   T   P   S   S   K   R   F   Q   P
ACT GGT ACT GGT GTG TTA ACT CCT TCT TCA AAG AGA TTT CAA CCA

                                540
    F   Q   Q   F   G   R   D   V   S   D   F   T   D   S   V
TTT CAA CAA TTT GGC CGT GAT GTT TCT GAT TTC ACT GAT TCC GTT

                                560
    R   D   P   K   T   S   E   I   L   D   I   S   P   C   S
CGA GAT CCT AAA ACA TCT GAA ATA TTA GAC ATT TCA CCT TGC TCT

                                570
    F   G   G   V   S   V   I   T   P   G   T   N   A   S   S
TTT GGG GGT GTA AGT GTA ATT ACA CCT GGA ACA AAT GCT TCA TCT

                                590
    E   V   A   V   L   Y   Q   D   V   N   C   T   D   V   S
GAA GTT GCT GTT CTA TAT CAA GAT GTT AAC TGC ACT GAT GTT TCT

                                600
    T   A   I   H   A   D   Q   L   T   P   A   W   R   I   Y

```

ACA GCA ATT CAT GCA GAT CAA CTC ACA CCA GCT TGG CGC ATA TAT

620

S T G N N V F Q T Q A G C L I
TCT ACT GGA AAC AAT GTA TTC CAG ACT CAA GCA GGC TGT CTT ATA

630

640

G A E H V D T S Y E C D I P I
GGA GCT GAG CAT GTT GAT ACT TCT TAT GAG TGC GAC ATT CCT ATT

650

G A G I C A S Y H T OC
GGA GCT GGC ATT TGT GCT AGT TAC CAT ACA TAA TGAGTCGAC

SEQ ID NO: 9799

SEQ ID NO: 9800

Translated Mol. Weight = 72525.52

FIGURE 66

1 10
M S D L D R C T T F
AAGCTTACAAAACAAA ATG AGT GAC CTT GAC CGG TGC ACC ACT TTT

20
D D V Q A P N Y T Q H T S S M
GAT GAT GTT CAA GCT CCT AAT TAC ACT CAA CAT ACT TCA TCT ATG

30 40
R G V Y Y P D E I F R S D T L
AGG GGG GTT TAC TAT CCT GAT GAA ATT TTT AGA TCA GAC ACT CTT

50
Y L T Q D L F L P F Y S N V T
TAT TTA ACT CAG GAT TTA TTT CTT CCA TTT TAT TCT AAT GTT ACA

60 70
G F H T I N H T F G N P V I P
GGG TTT CAT ACT ATT AAT CAT ACG TTT GGC AAC CCT GTC ATA CCT

80
F K D G I Y F A A T E K S N V
TTT AAG GAT GGT ATT TAT TTT GCT GCC ACA GAG AAA TCA AAT GTT

90 100
V R G W V F G S T M N N K S Q
GTC CGT GGT TGG GTT TTT GGT TCT ACC ATG AAC AAC AAG TCA CAG

110
S V I I I N N S T N V V I R A
TCG GTG ATT ATT ATT AAC AAT TCT ACT AAT GTT GTT ATA CGA GCA

120 130
C N F E L C D N P F F A V S K
TGT AAC TTT GAA TTG TGT GAC AAC CCT TTC TTT GCT GTT TCT AAA

140
P M G T Q T H T M I F D N A F
CCC ATG GGT ACA CAG ACA CAT ACT ATG ATA TTC GAT AAT GCA TTT

150 160
N C T F E Y I S D A F S L D V

AAT TGC ACT TTC GAG TAC ATA TCT GAT GCC TTT TCG CTT GAT GTT
 170
 S E K S G N F K H L R E F V F
 TCA GAA AAG TCA GGT AAT TTT AAA CAC TTA CGA GAG TTT GTG TTT
 180 190
 K N K D G F L Y V Y K G Y Q P
 AAA AAT AAA GAT GGG TTT CTC TAT GTT TAT AAG GGC TAT CAA CCT
 200
 I D V V R D L P S G F N T L K
 ATA GAT GTA GTT CGT GAT CTA CCT TCT GGT TTT AAC ACT TTG AAA
 210 220
 P I F K L P L G I N I T N F R
 CCT ATT TTT AAG TTG CCT CTT GGT ATT AAC ATT ACA AAT TTT AGA
 230
 A I L T A F S P A Q D I W G T
 GCC ATT CTT ACA GCC TTT TCA CCT GCT CAA GAC ATT TGG GGC ACG
 240 250
 S A A A Y F V G Y L K P T T F
 TCA GCT GCA GCC TAT TTT GTT GGC TAT TTA AAG CCA ACT ACA TTT
 260
 M L K Y D E N G T I T D A V D
 ATG CTC AAG TAT GAT GAA AAT GGT ACA ATC ACA GAT GCT GTT GAT
 270 280
 C S Q N P L A E L K C S V K S
 TGT TCT CAA AAT CCA CTT GCT GAA CTC AAA TGC TCT GTT AAG AGC
 290
 F E I D K G I Y Q T S N F R V
 TTT GAG ATT GAC AAA GGA ATT TAC CAG ACC TCT AAT TTC AGG GTT
 300 310
 V P S G D V V R F P N I T N L
 GTT CCC TCA GGA GAT GTT GTG AGA TTC CCT AAT ATT ACA AAC TTG
 320
 C P F G E V F N A T K F P S V
 TGT CCT TTT GGA GAG GTT TTT AAT GCT ACT AAA TTC CCT TCT GTC
 330 340
 Y A W E R K K I S N C V A D Y
 TAT GCA TGG GAG AGA AAA AAA ATT TCT AAT TGT GTT GCT GAT TAC
 350
 S V L Y N S T F F S T F K C Y
 TCT GTG CTC TAC AAC TCA ACA TTT TTT TCA ACC TTT AAG TGC TAT
 360 370
 G V S A T K L N D L C F S N V
 GGC GTT TCT GCC ACT AAG TTG AAT GAT CTT TGC TTC TCC AAT GTC
 380
 Y A D S F V V K G D D V R Q I
 TAT GCA GAT TCT TTT GTA GTC AAG GGA GAT GAT GTA AGA CAA ATA
 390 400

119/199

A P G Q T G V I A D Y N Y K L
 GCG CCA GGG CAA ACT GGT GTT ATT GCT GAT TAT AAT TAT AAA TTG
 410
 P D D F M G C V L A W N T R N
 CCA GAT GAT TTC ATG GGT TGT GTC CTT GCT TGG AAT ACT AGG AAC
 420 430
 I D A T S T G N Y N Y K Y R Y
 ATT GAT GCT ACT TCA ACT GGT AAT TAT AAT TAT AAA TAT AGG TAT
 440
 L R H G K L R P F E R D I S N
 CTT AGA CAT GGC AAG CTT AGG CCC TTT GAG AGA GAC ATA TCT AAT
 450 460
 V P F S P D G K P C T P P A L
 GTG CCT TTC TCC CCT GAT GGC AAA CCT TGC ACC CCA CCT GCT CTT
 470
 N C Y W P L N D Y G F Y T T T
 AAT TGT TAT TGG CCA TTA AAT GAT TAT GGT TTT TAC ACC ACT ACT
 480 490
 G I G Y Q P Y R V V V L S F E
 GGC ATT GGC TAC CAA CCT TAC AGA GTT GTA GTA CTT TCT TTT GAA
 500
 L L N A P A T V C G P K L S T
 CTT TTA AAT GCA CCG GCC ACG GTT TGT GGA CCA AAA TTA TCC ACT
 510 520
 D L I K N Q C V N F N F N G L
 GAC CTT ATT AAG AAC CAG TGT GTC AAT TTT AAT TTT AAT GGA CTC
 530
 T G T G V L T P S S K R F Q P
 ACT GGT ACT GGT GTG TTA ACT CCT TCT TCA AAG AGA TTT CAA CCA
 540 550
 F Q Q F G R D V S D F T D S V
 TTT CAA CAA TTT GGC CGT GAT GTT TCT GAT TTC ACT GAT TCC GTT
 560
 R D P K T S E I L D I S P C S
 CGA GAT CCT AAA ACA TCT GAA ATA TTA GAC ATT TCA CCT TGC TCT
 570 580
 F G G V S V I T P G T N A S S
 TTT GGG GGT GTA AGT GTA ATT ACA CCT GGA ACA AAT GCT TCA TCT
 590
 E V A V L Y Q D V N C T D V S
 GAA GTT GCT GTT CTA TAT CAA GAT GTT AAC TGC ACT GAT GTT TCT
 600 610
 T A I H A D Q L T P A W R I Y
 ACA GCA ATT CAT GCA GAT CAA CTC ACA CCA GCT TGG CGC ATA TAT
 620
 S T G N N V F Q T Q A G C L I
 TCT ACT GGA AAC AAT GTA TTC CAG ACT CAA GCA GGC TGT CTT ATA

120/199

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      630
G   A   E   H   V   D   T   S   Y   E   C   D   I   P   I
GGA GCT GAG CAT GTC GAC ACT TCT TAT GAG TGC GAC ATT CCT ATT

      650
G   A   G   I   C   A   S   Y   H   T   V   S   L   L   R
GGA GCT GGC ATT TGT GCT AGT TAC CAT ACA GTT TCT TTA TTA CGT

      660
S   T   S   Q   K   S   I   V   A   Y   T   M   S   L   G
AGT ACT AGC CAA AAA TCT ATT GTG GCT TAT ACT ATG TCT TTA GGT

      680
A   D   S   S   I   A   Y   S   N   N   T   I   A   I   P
GCT GAT AGT TCA ATT GCT TAC TCT AAT AAC ACC ATT GCT ATA CCT

      690
T   N   F   S   I   S   I   T   T   E   V   M   P   V   S
ACT AAC TTT TCA ATT AGC ATT ACT ACA GAA GTA ATG CCT GTT TCT

      710
M   A   K   T   S   V   D   C   N   M   Y   I   C   G   D
ATG GCT AAA ACC TCC GTA GAT TGT AAT ATG TAC ATC TGC GGA GAT

      720
S   T   E   C   A   N   L   L   L   Q   Y   G   S   F   C
TCT ACT GAA TGT GCT AAT TTG CTT CTC CAA TAT GGT AGC TTT TGC

      740
T   Q   L   N   R   A   L   S   G   I   A   A   E   Q   D
ACA CAA CTA AAT CGT GCA CTC TCA GGT ATT GCT GCT GAA CAG GAT

      750
R   N   T   R   E   V   F   A   Q   V   K   Q   M   Y   K
CGC AAC ACA CGT GAA GTG TTC GCT CAA GTC AAA CAA ATG TAC AAA

      770
T   P   T   L   K   Y   F   G   G   F   N   F   S   Q   I
ACC CCA ACT TTG AAA TAT TTT GGT GGT TTT AAT TTT TCA CAA ATA

      780
L   P   D   P   L   K   P   T   K   R   S   F   I   E   D
TTA CCT GAC CCT CTA AAG CCA ACT AAG AGG TCT TTT ATT GAG GAC

      800
L   L   F   N   K   V   T   L   A   D   A   G   F   M   K
TTG CTC TTT AAT AAG GTG ACA CTC GCT GAT GCT GGC TTC ATG AAG

      810
Q   Y   G   E   C   L   G   D   I   N   A   R   D   L   I
CAA TAT GGC GAA TGC CTA GGT GAT ATT AAT GCT AGG GAC CTC ATT

      830
C   A   Q   K   F   N   G   L   T   V   L   P   P   L   L
TGT GCG CAG AAG TTC AAT GGA CTT ACA GTG TTG CCA CCT CTG CTC

      840
T   D   D   M   I   A   A   Y   T   A   A   L   V   S   G
ACT GAT GAT ATG ATT GCT GCC TAC ACT GCT GCT CTA GTT AGT GGT

      860
T   A   T   A   G   W   T   F   G   A   G   A   A   L   Q
ACT GCC ACT GCT GGA TGG ACA TTT GGT GCT GGC GCT GCT CTT CAA

```

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      870                                     880
    I   P   F   A   M   Q   M   A   Y   R   F   N   G   I   G
    ATA CCT TTT GCT ATG CAA ATG GCA TAT AGG TTC AAT GGC ATT GGA

                                     890
    V   T   Q   N   V   L   Y   E   N   Q   K   Q   I   A   N
    GTT ACC CAA AAT GTT CTC TAT GAG AAC CAA AAA CAA ATC GCC AAC

      900                                     910
    Q   F   N   K   A   I   S   Q   I   Q   E   S   L   T   T
    CAA TTT AAC AAG GCG ATT AGT CAA ATT CAA GAA TCA CTT ACA ACA

                                     920
    T   S   T   A   L   G   K   L   Q   D   V   V   N   Q   N
    ACA TCA ACT GCA TTG GGC AAG CTG CAA GAC GTT GTT AAC CAG AAT

      930                                     940
    A   Q   A   L   N   T   L   V   K   Q   L   S   S   N   F
    GCT CAA GCA TTA AAC ACA CTT GTT AAA CAA CTT AGC TCT AAT TTT

                                     950
    G   A   I   S   S   V   L   N   D   I   L   S   R   L   D
    GGT GCA ATT TCA AGT GTG CTA AAT GAT ATC CTT TCG CGA CTT GAT

      960                                     970
    K   V   E   A   E   V   Q   I   D   R   L   I   T   G   R
    AAA GTC GAG GCG GAG GTA CAA ATT GAC AGG TTA ATT ACA GGC AGA

                                     980
    L   Q   S   L   Q   T   Y   V   T   Q   Q   L   I   R   A
    CTT CAA AGC CTT CAA ACC TAT GTA ACA CAA CAA CTA ATC AGG GCT

      990                                     1000
    A   E   I   R   A   S   A   N   L   A   A   T   K   M   S
    GCT GAA ATC AGG GCT TCT GCT AAT CTT GCT GCT ACT AAA ATG TCT

                                     1010
    E   C   V   L   G   Q   S   K   R   V   D   F   C   G   K
    GAG TGT GTT CTT GGA CAA TCA AAA AGA GTT GAC TTT TGT GGA AAG

      1020                                     1030
    G   Y   H   L   M   S   F   P   Q   A   A   P   H   G   V
    GGC TAC CAC CTT ATG TCC TTC CCA CAA GCA GCC CCG CAT GGT GTT

                                     1040
    V   F   L   H   V   T   Y   V   P   S   Q   E   R   N   F
    GTC TTC CTA CAT GTC ACG TAT GTG CCA TCC CAG GAG AGG AAC TTC

      1050                                     1060
    T   T   A   P   A   I   C   H   E   G   K   A   Y   F   P
    ACC ACA GCG CCA GCA ATT TGT CAT GAA GGC AAA GCA TAC TTC CCT

                                     1070
    R   E   G   V   F   V   F   N   G   T   S   W   F   I   T
    CGT GAA GGT GTT TTT GTG TTT AAT GGC ACT TCT TGG TTT ATT ACA

      1080                                     1090
    Q   R   N   F   F   S   P   Q   I   I   T   T   D   N   T
    CAG AGG AAC TTC TTT TCT CCA CAA ATA ATT ACT ACA GAC AAT ACA

                                     1100
    F   V   S   G   N   C   D   V   V   I   G   I   I   N   N

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122/199

TTT GTC TCA GGA AAT TGT GAT GTC GTT ATT GGC ATC ATT AAC AAC
1110 1120
T V Y D P L Q P E L D S F K E
ACA GTT TAT GAT CCT CTG CAA CCT GAG CTT GAC TCA TTC AAA GAA
1130
E L D K Y F K N H T S P D V D
GAG CTG GAC AAG TAC TTC AAA AAT CAT ACA TCA CCA GAT GTT GAT
1140 1150
F G D I S G I N A S V V N I Q
TTT GGC GAC ATT TCA GGC ATT AAC GCT TCT GTC GTC AAC ATT CAA
1160
K E I D R L N E V A K N L N E
AAA GAA ATT GAC CGC CTC AAT GAG GTC GCT AAA AAT TTA AAT GAA
1170 1180
S L I D L Q E L G K Y E Q Y I
TCA CTC ATT GAC CTT CAA GAA TTG GGA AAA TAT GAG CAA TAT ATT
1183
K W P OC
AAA TGG CCT TAA TGAGTCGAC

SEQ ID NO: 9801

SEQ ID NO: 9802

Translated Mol. Weight = 131315.20

FIGURE 67

FIGURE 67A

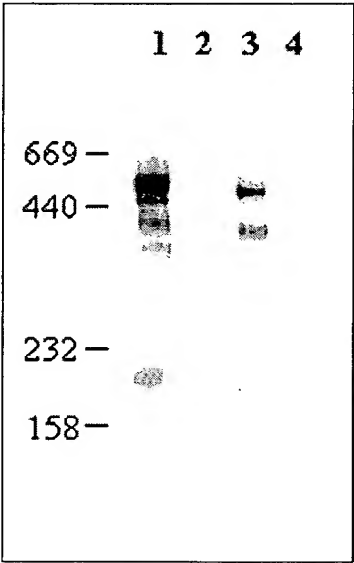


FIGURE 67B

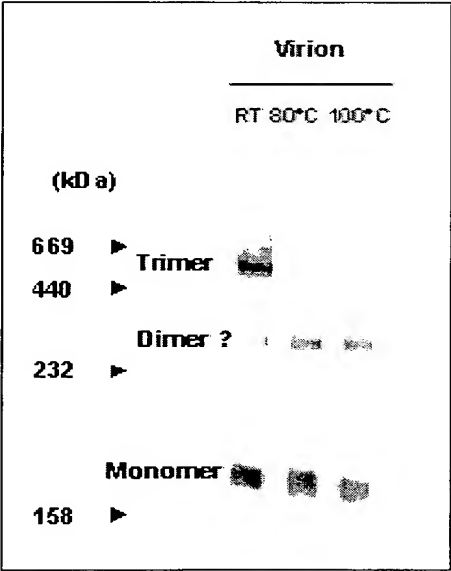


FIGURE 68

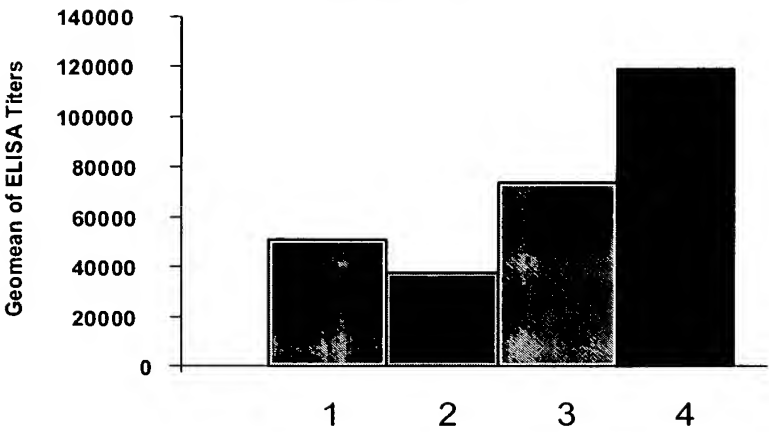


FIGURE 69

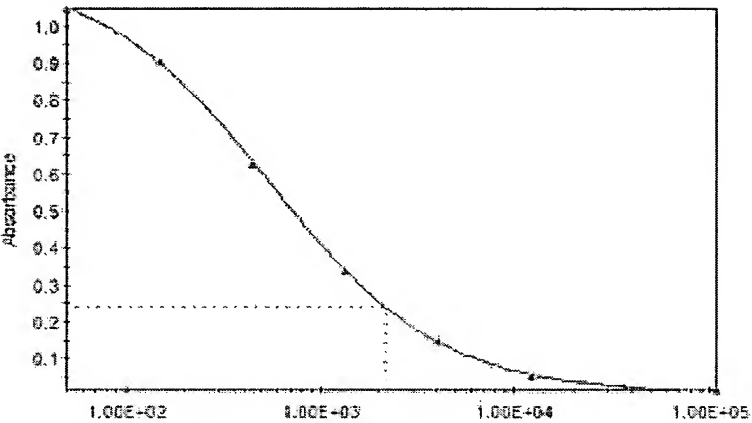


FIGURE 70

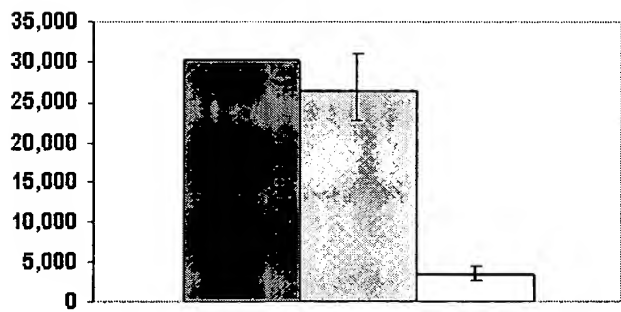


FIGURE 71

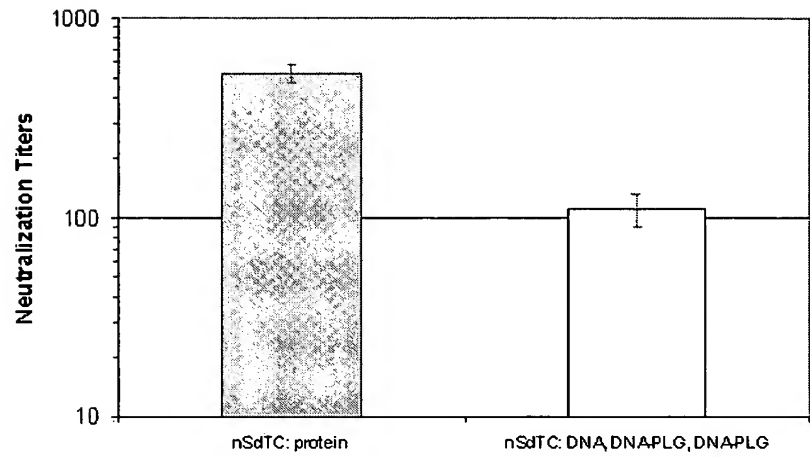


FIGURE 72

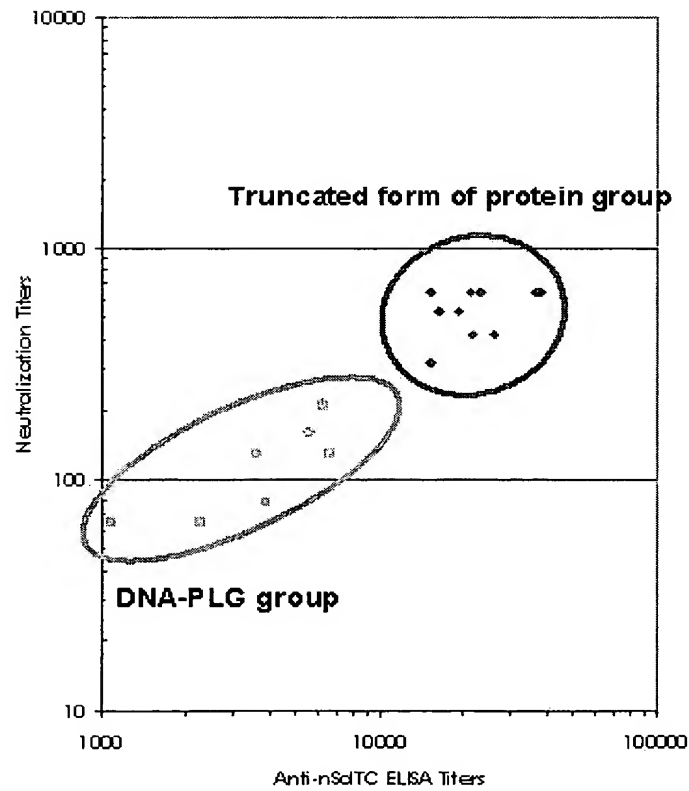


FIGURE 73

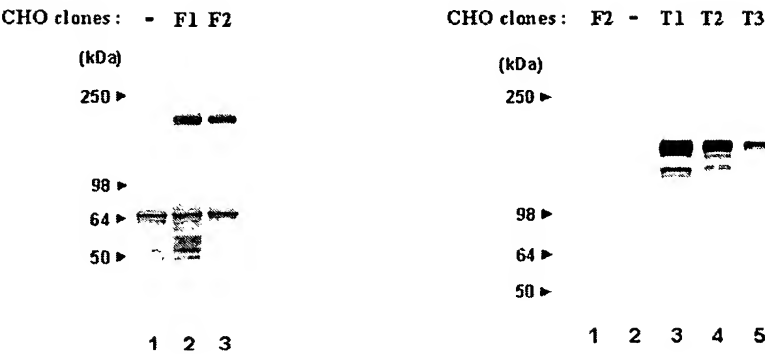


FIGURE 74

FIGURE 74A



FIGURE 74B

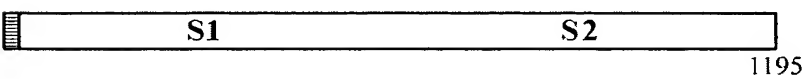


FIGURE 75

FIGURE 75A

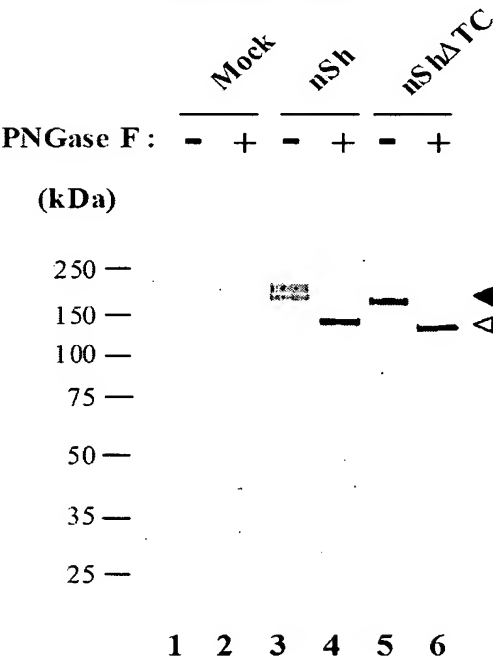


FIGURE 75B

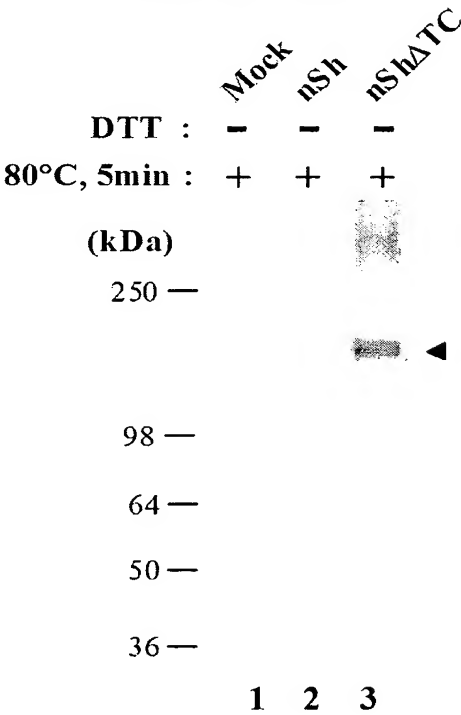


FIGURE 76

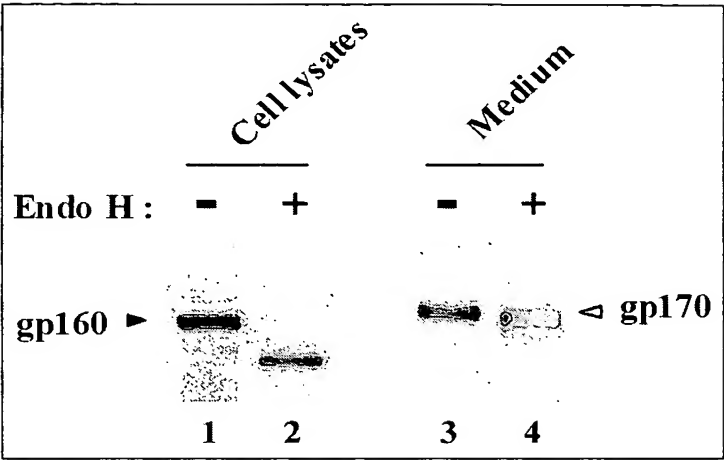


FIGURE 77

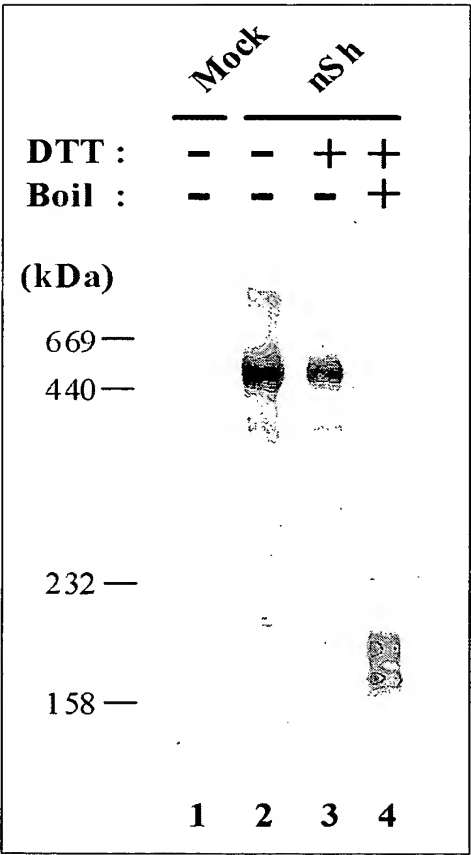
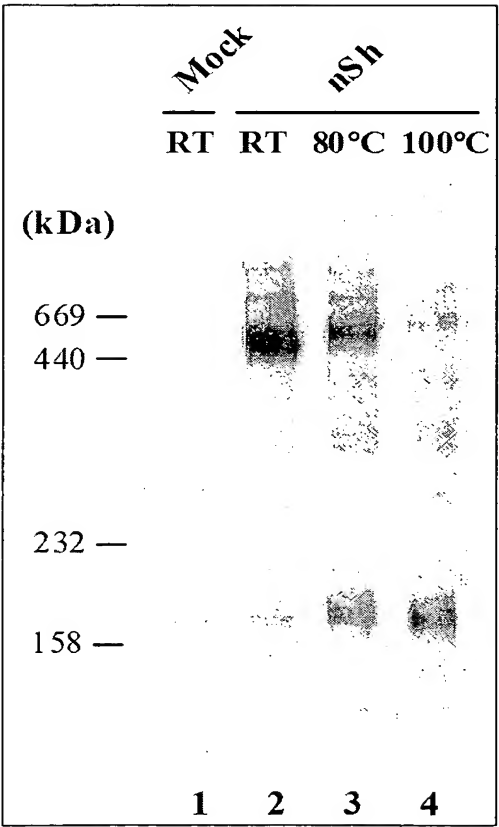


FIGURE 78



127/199

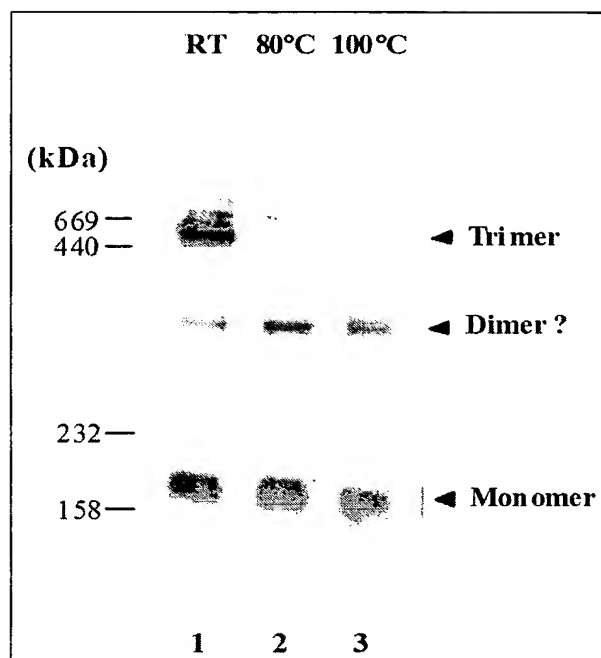
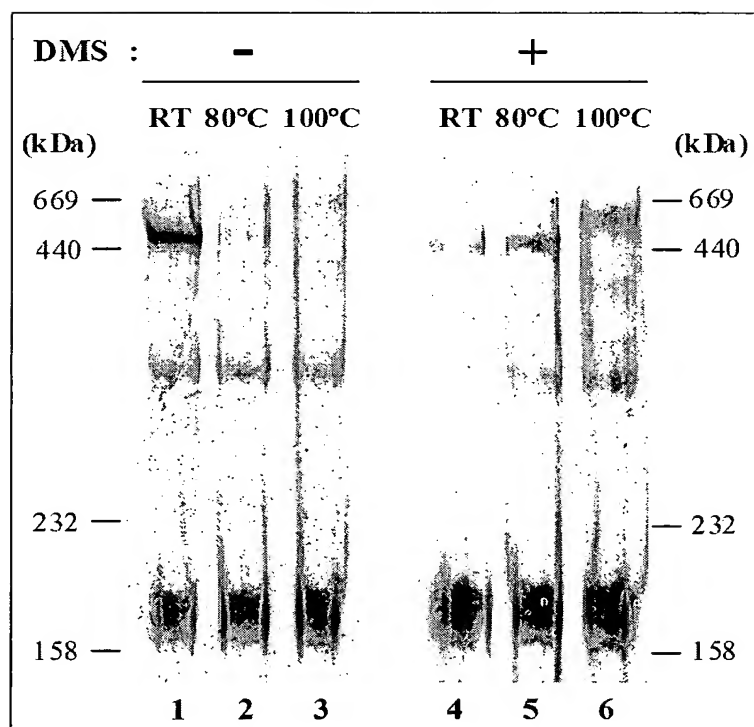
FIGURE 79**FIGURE 80**

FIGURE 81

RT 80°C 100°C

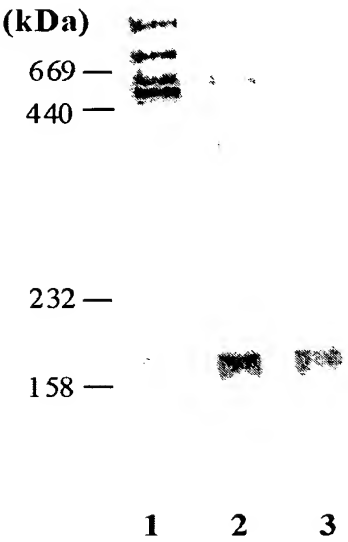


FIGURE 82

RT 80°C 100°C

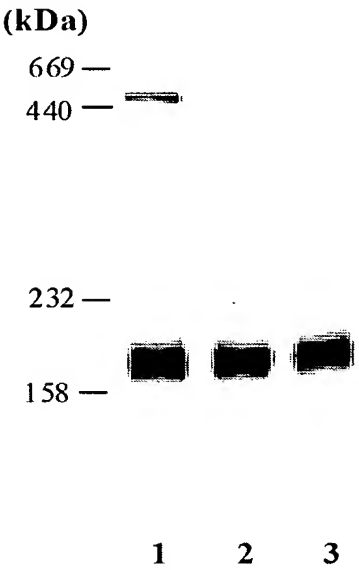


FIGURE 83

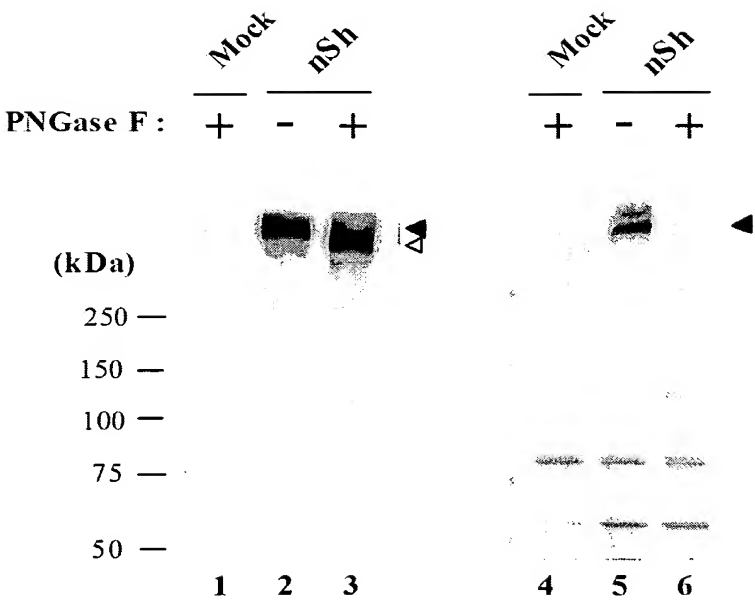


FIGURE 84

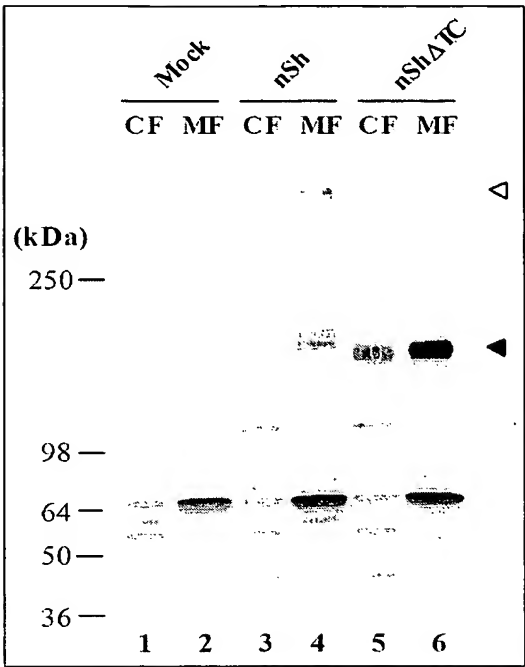


FIGURE 85

FIGURE 85A

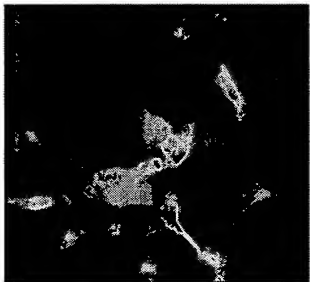


FIGURE 85B

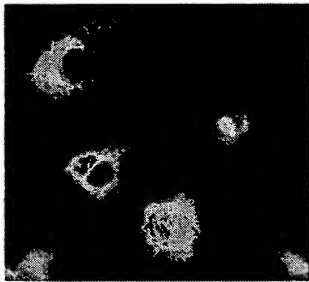


FIGURE 85C

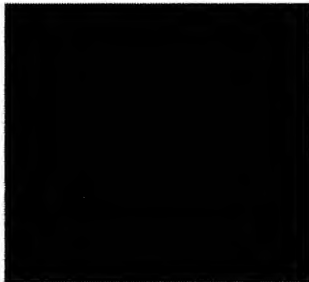


FIGURE 85D

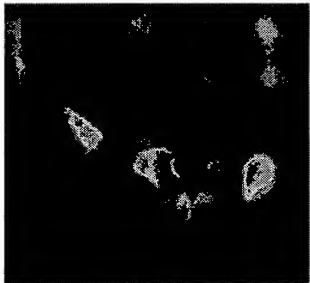


FIGURE 85E

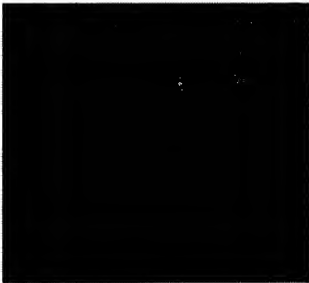


FIGURE 85F

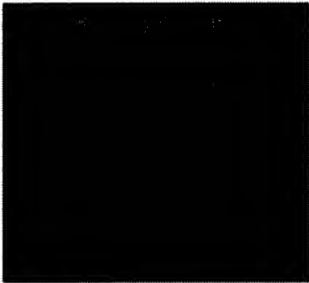


FIGURE 86

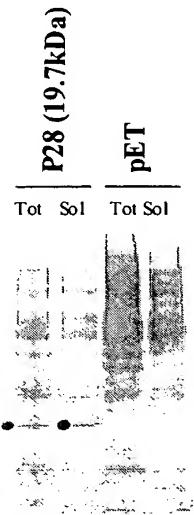


FIGURE 87

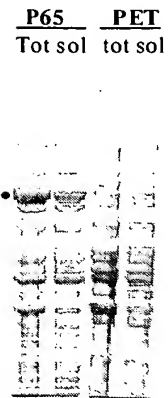


FIGURE 88

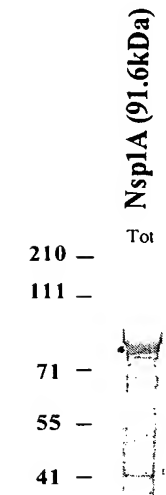


FIGURE 89

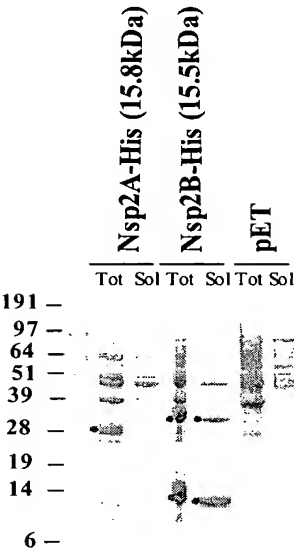


FIGURE 90

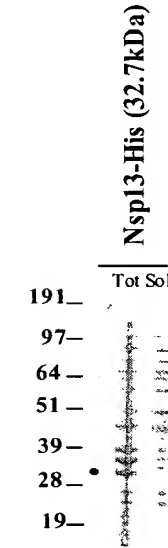


FIGURE 91

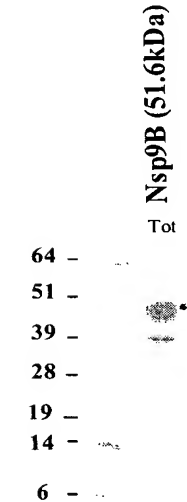


FIGURE 92

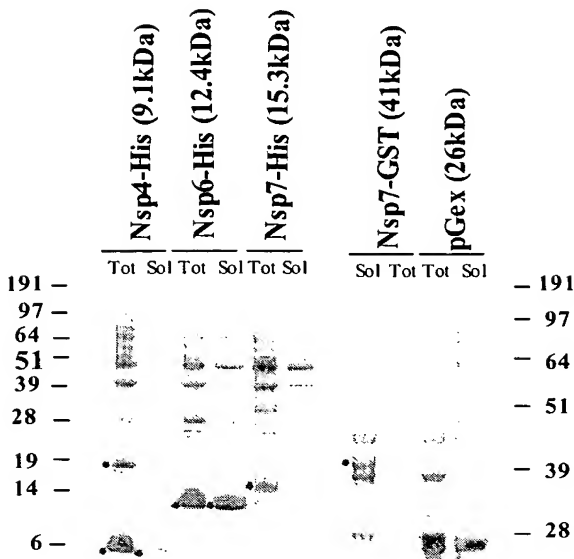


FIGURE 93

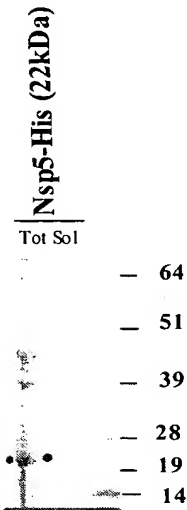


FIGURE 94

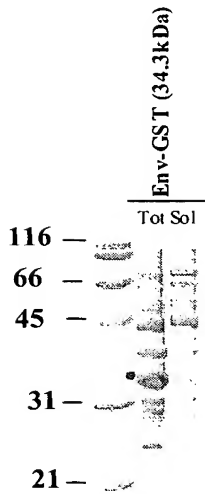


FIGURE 95

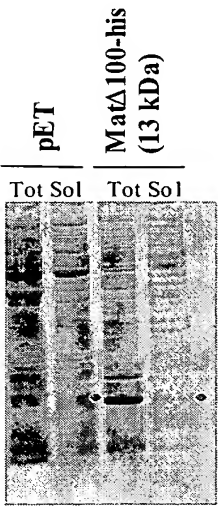


FIGURE 96

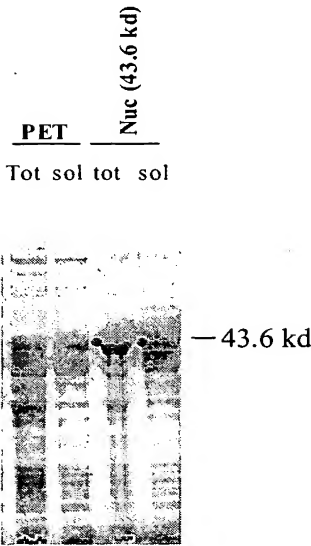


FIGURE 97

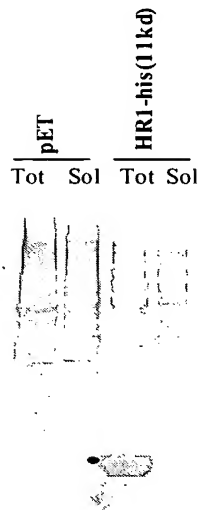


FIGURE 98

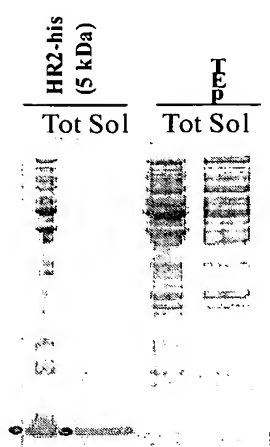


FIGURE 99

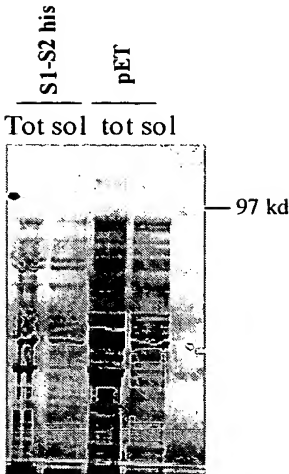


FIGURE 100

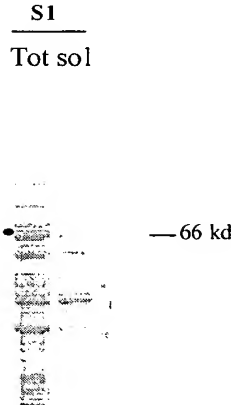


FIGURE 101

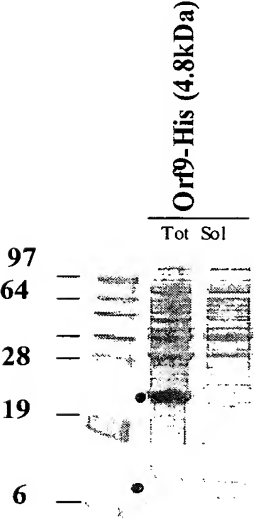


FIGURE 102

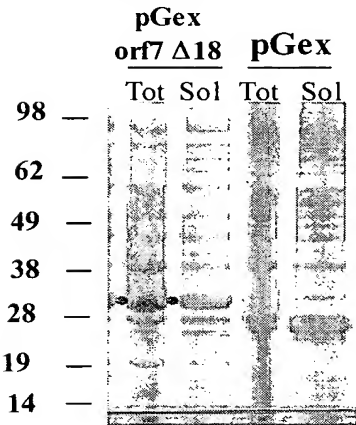


FIGURE 103

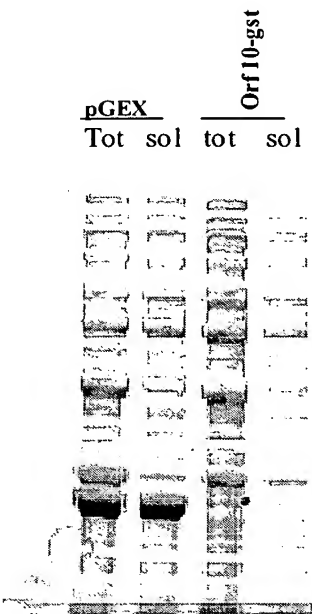


FIGURE 104

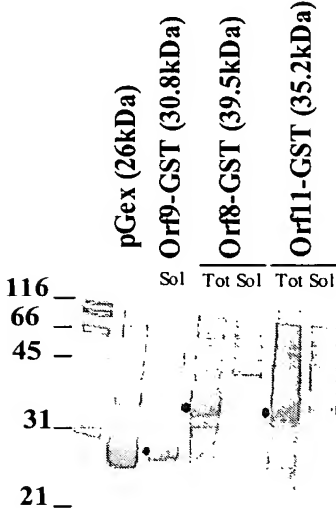


FIGURE 105

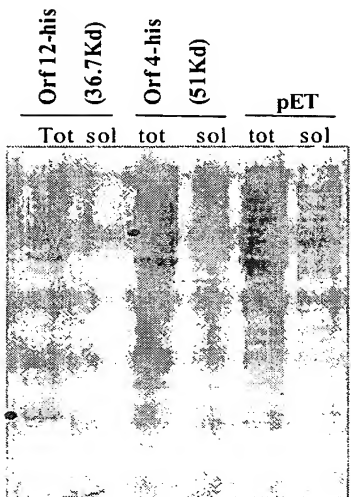


FIGURE 106

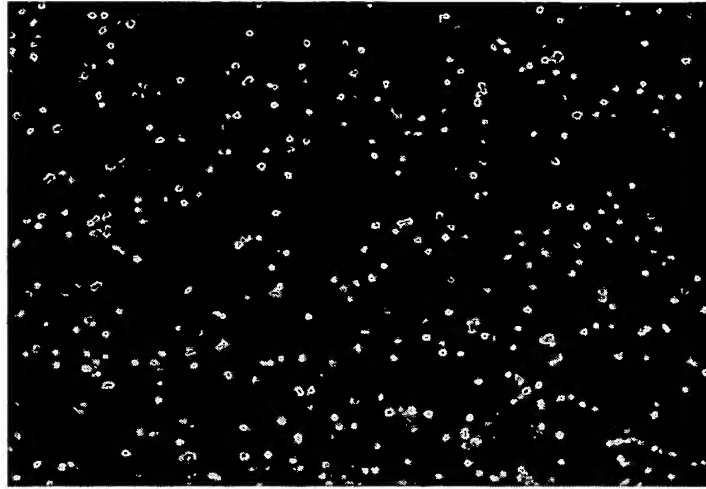


FIGURE 107

FIGURE 107A

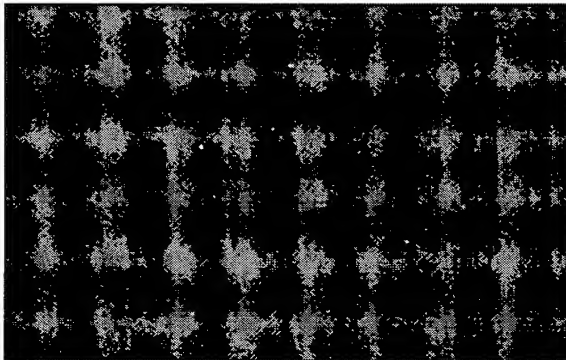


FIGURE 107B

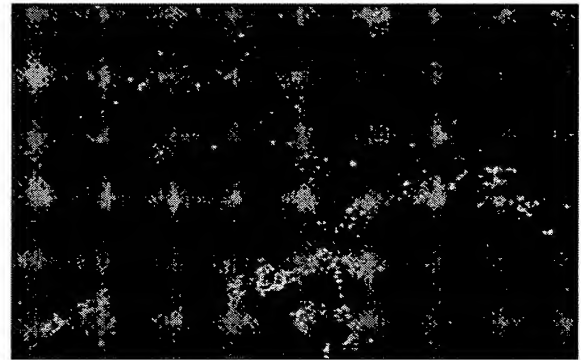


FIGURE 108

FIGURE 108A



FIGURE 108B



FIGURE 109

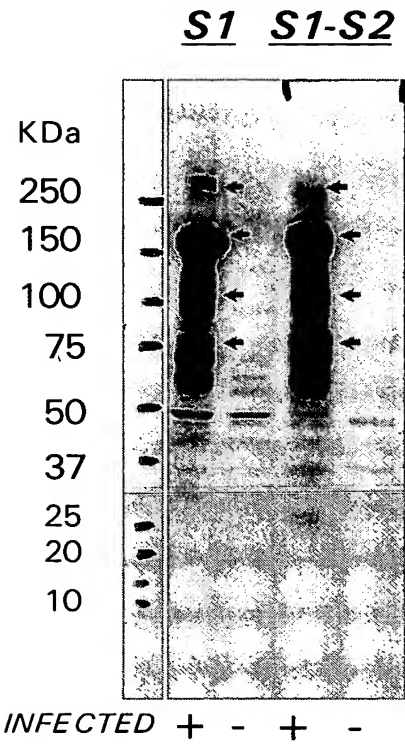


FIGURE 110

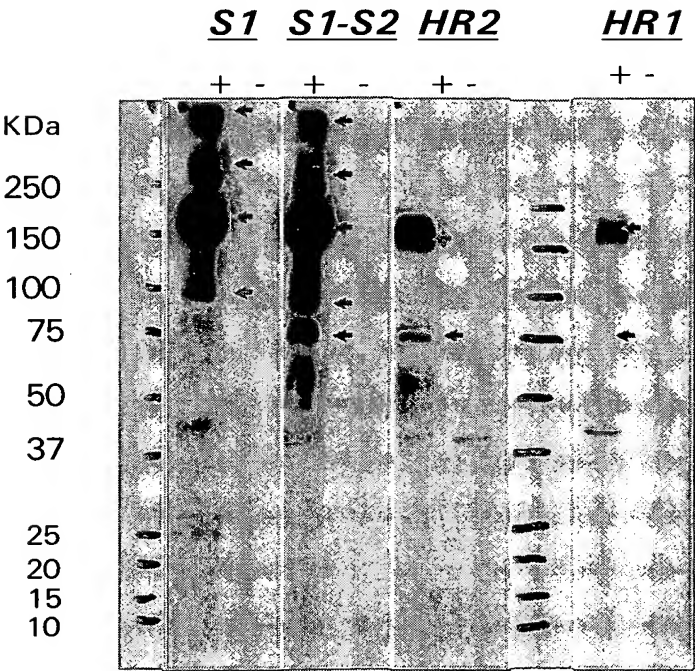


FIGURE 111

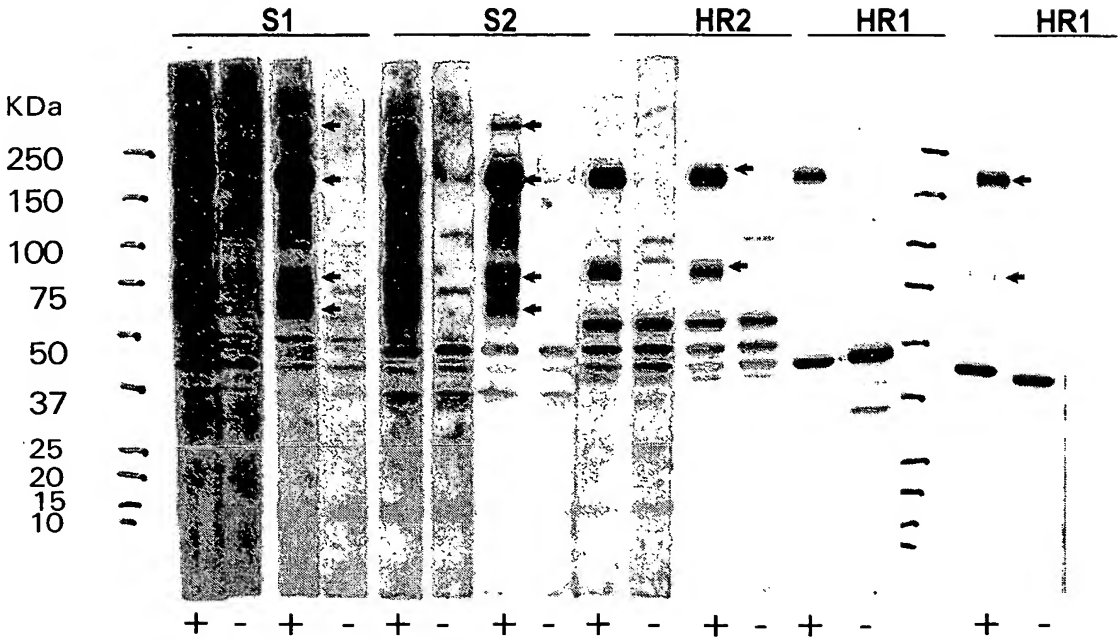


FIGURE 112

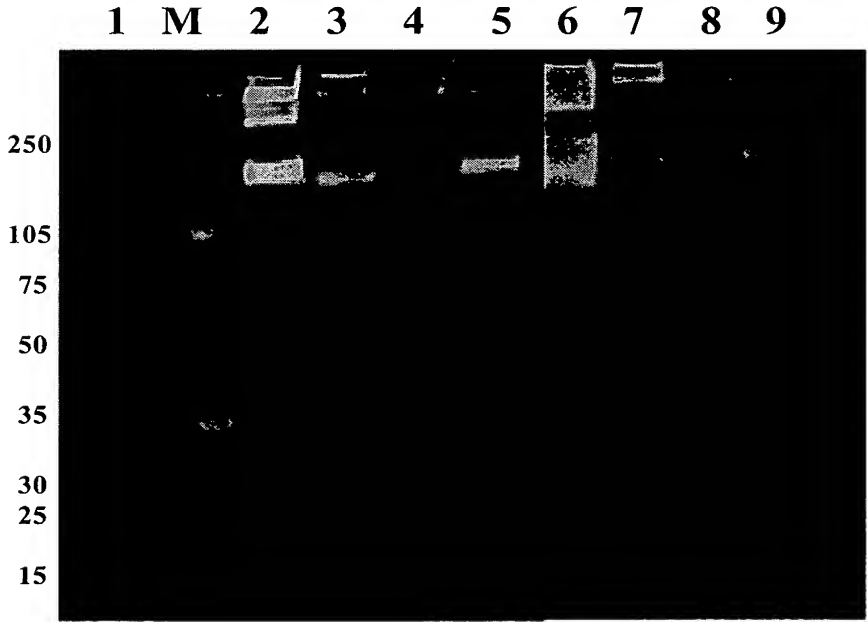


FIGURE 113**5'3' Frame 1**

PKDMTYVDSSL-WVS-ITKSMVTLICLSPAKKLFVTFVRGLALM-RAVMQLEMLWVLTYLS
S-DFLQVLT--LYRLVMLTLKITQNSPELMHKPPPVSSSLNILYHSCIKACPGM-CVLR-YK
CSVIH-KDCQTESCSSFGRMALSLHQ-STLSRLDLKERVVCVTNVQLAFLHQLMPAGII
LWVLTSITHL-LMFSSGGFTGNLSE-P-PTLPGTWKCTCGLVVML

5'3' Frame 2

QRT-PT-THLYDGFQNELPSQWLP-YVYHPRRSYSSRSCVDWL-CRGLSCN-RCCGY-PTS
PARIFYRC-LSSCTDWLC-H-K-HKIHQS-CTNLHQ-AV-TSYTTHV-RLALECSAY-DST
NAQ-YTERIVRQSRVRPLGAWL-AYINEVLCQDWT-KNVLSV-QTCNLLFYFIRYLCLLES
FCGF-LCL-PIYD-CSAVGALRVTFQSNHDQHCQVHGNAHVG-L-C

5'3' Frame 3

KGHDLRRLISMGMFYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPL
QLGFSTGVNLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLMYKGLPWNVVRKIVQ
MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWNH
SVGFDYVYNPFMIDVQQWGLYG-PFRVTMTNIARYMEMHMMWASCD

3'5' Frame 1

-HHN-PTCAFPCTWQCWSWLL-KVTRKAPTAEHQS-MGYRHSQNPQNDSSRHKYLK-KSK
LHVCHTDNTFFQVQS-QSTSLM-AQSHAPKGRTRLCLTILSVYH-AFVLS-YALHSRASLY
T-VV-DV-TAHWWRFVH-LW-ILCYFQCQHNQSVQLLS-HL-KILAGEVG-YPQHL-LHDS
PLHQSQSTHERDE-LLRG--TY-GNH-LGNSF-NPS-R-VYVGHVLW

3'5' Frame 2

SITTSPHVHFHVPGNVGHGYSERLPVKPPLLNNHKKWVIDIVKTHRMIPAGISI--SRKAS
CTFVTQTTRSFRSNLDKVLH-CKLKAMRPKDEHDSV-QSFQCITEHLYYLNTHYIPGQAFI
HEWYKMFKLLTGGLCINSGEFCVIFSVNITSRYSY-VNTRKS-LER-VSTHSISSCMTA
LYIKANPRTNVTNSFFAGDKHIRVTIDLVIHFETHHRDEST-VMSF

3'5' Frame 3

ASQLAHMCISMYLAMLVMVTLKGYP-SPHC-TSIINGL-T-SKPTE-FQQA-VSDEVEKQV
ARLSHRQHVLSGPILTKYFIDVSSKPCAQRTNTTSLSDNPFSVLSICTILIRTTFQGKPLY
MSGIRCLNCSLVEVCALTLVNFVLFVSST-PVGTATKLPVENPSWRGRLVPTASLVA-QP
STSKPIHART-RIASSRVINILG-PLTW-FILKPIIEMSLRRSCPL

FIGURE 114**5'3' Frame 1**

YRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQLGF
STGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLI

5'3' Frame 2

TVDSSL-WVSK-ITKSMVTLICLSPAKKLFVTFVRGLALM-RAVMQLEMLWVLTYLSS-DF
LQVLT--LYRLVMLTLKITQNSPELMQNLHQVTSLNILY

5'3' Frame 3

P-THLYDGFQNELPSQWLP-YVYHPRRSYSSRSCVDWL-CRGLSCN-RCCGY-PTSPARIF
YRC-LSSCTDWLC-H-K-HRIHQSC-CKTSTR-PV-TSYT

3'5' Frame 1

GIRCLNWSPGGGFALTIVNSVLFVSVST-PVGTATKLTPVENPSWRGRLVPTASLVA-QPST
SKPIHART-RIASSRVINILG-PLTW-FILKPIIEMSLR

3'5' Frame 2

V-DV-TGHLVEVLH-LW-ILCYFQCQHNQSVQLLS-HL-KILAGEVG-YPQHL-LHDSPLH
QSQSTHERDE-LLRG--TY-GNH-LGNSF-NPS-R-VYG

3'5' Frame 3

YKMFKLVTWWRFCINSGEFCVIFSVNITSRYSY-VNTRCKS-LER-VSTHSISSCMTALYI
KANPRNTVNTNSFFAGDKHIRVTIDLVIHFETHHRDESTV

FIGURE 115

Section 151

(5851) 5851 5860 5870 5889
 (5675) LTNYELSVINARIRAKHYVYIGDPAQLPAPRVLLCKGTL
 (5247) LTNYELSFINGKINYCYVYVYVGDPAQLPAPRTLLNG-ST
 (5762) LTNYELSVINSRVSAKHYVYIGDPAQLPAPRVLLNKGTL
 (1) -----
 (5851) LTNYELSVINARI AKHYVYIGDPAQLPAPRVLLNKGTL

Section 152

(5890) 5890 5900 5910 5928
 (5714) EPKYFNTVTKLMCCCLGPDIFLGTCYRCPKEIVDTVSAIV
 (5285) SPKDYNVVTNLMVCVKPDIFELAKCYRCPKEIVDTVSTLV
 (5801) EPRYFNSVTKLMCCCLGPDIFLGTCYRCPKEIVDTVSAIV
 (1) -----
 (5890) EPKYFNSVTKLMCCCLGPDIFLGTCYRCPKEIVDTVSAIV

Section 153

(5929) 5929 5940 5950 5967
 (5753) YENKLKAKNESSSLCFKVYYKG---VTTHESSSAVNMQQ
 (5324) YDCKFIANNPESRECFKVIHNGNSDVGHESGSAYNTO
 (5840) YENKLKAKNDNSSMCFKVYYKG---QTTHESSSAVNMQQ
 (1) -----
 (5929) YDNKLKAKND SSLCFKVYYKG TTHESSSAVNMQQ

Section 154

(5968) 5968 5980 5990 6006
 (5789) IYLLINKELKANPLWHKAVFISPYNSQNEAAKRVLGLQTO
 (5363) LEFMKDFVCRNKQWREAFISPYNAMNQRAYRMLGLINVO
 (5876) IHLISKELKANPSWSNAVEFISPYNSQNYVAKRVLGLQTO
 (1) -----
 (5968) IHLI KFLKANP W AVFISPYNSQNF AKRVLGLQTO

Section 155

(6007) 6007 6020 6030 6045
 (5828) TVDSAQGSEYDYVIYSQTAETAHSVNVNRENVAITRAKK
 (5402) TVDSSQGSEYDYVLECVTADSQHALNENRENVAITRAKK
 (5915) TVDSAQGSEYDEVYYSQTAETAHSVNVNRENVAITRAKK
 (1) -----
 (6007) TVDSAQGSEYDYVIYSQTAETAHSVNVNRENVAITRAKK

Section 156

(6046) 6046 6060 6070 → 6084
 (5867) GILCVMSNMQLFEALQFTTLTLDKMPQAVETRVQCSTNL
 (5441) GILVVMRQRDELYSALKFTELDSETS-----LQG--TGL
 (5954) GILCVMSNMQLFESLNFTTLTLDKIN---NPRLOQTTLNL
 (1) -----
 (6046) GILCVMSNMQLFESLNFTTLTLDKI RLCQSTNL

START

FIGURE 115 (contd.)**Section 157**

(6085) 6085 6090 6100 6110 6123
 (5906) FKDCSKSYSGYHPAHAPSEFLAVDDKYKATGDLAVCLGIG
 (5473) FKICNKEESGVHPAYAVITTKALAAATYKVNDELAAALVNVE
 (5990) FKDCSRSYVGYHPAHAPSEFLAVDDKYKVGGDLAVCLNVA
 (1) -----
 (6085) FKDCSKSYSGYHPAHAPSEFLAVDDKYKV GDLAVCLNVA

Section 158

(6124) 6124 6130 6140 6150 6162
 (5945) D-SAVTYSRLISLMGFKLDVTLDGYCNLFITRDEAIKRV
 (5512) AGSETTYKHLISLIGFKMSVNVESCHNMFITRDEAIKRV
 (6029) D-SAVTYSRLISLMGFKLDVTLDGYCNLFITRDEAIKRV
 (1) --KGHDLRRLISLMGFKLDVTLDGYCNLFITRDEAIKRV
 (6124) D SAVTYSRLISLMGFKLDVTLDGYCNLFITRDEAIKRV

Section 159

(6163) 6163 6170 6180 6190 6201
 (5983) RAWVGFDASGAHAIRDSIGTNPLQLGFSTGIDFVVEAT
 (5551) RGVGFDVEGAHACGTNIGTNLPLQMGFSTGADEFVVTRE
 (6067) RAWVGFDASGAHAIRDSIGTNPLQLGFSTGIDFVVEAT
 (38) RAWVGFDVEGAHAIRDSIGTNPLQLGFSTGIDFVVEAT
 (6163) RAWVGFDVEGAHAIRDSIGTNPLQLGFSTGIDFVVEAT

Section 160

(6202) 6202 6210 6220 6230 6240
 (6022) GLFADRDGYSPKKAVAKAPPGEQFKHLIPLMSRGQPDV
 (5590) GLVDTSIGNNPEPMNSKAPPGEQFNHLIRVLENSAKPWHV
 (6106) GMFAERDGYVPKKAAABAPPGEQFKHLIPLMSRGQPDV
 (77) GYMDTENNTKETRYNACTSTSEQFKHLIPLMYKGLPWHV
 (6202) GLVDTRDGY FKKVNAKAPPGEQFKHLIPLMSRGQPDV

Section 161

(6241) 6241 6250 6260 6279
 (6061) VRPRIVQMLADHLIDLSDCVVLVTWAANFELTCLRYFAK
 (5629) VRPRIVQMLADMLCNVSDCVVFTWCHGLELTTLRYFVK
 (6145) VRIRIVQMLSDHLADLADSVLVTWAASFELTCLRYFAK
 (116) VRIKIVQMLSDTLKGLSDRVVFWLWAGFELTCLRYFVK
 (6241) VRPRIVQMLADHL IDSDCVVLVTWAHGFELTCLRYFVK

Section 162

(6280) 6280 6290 6300 6318
 (6100) VGREISCCNVCTKRATAYNSRTGYYGCWRHNSVTCLYLYNP
 (5668) IGKE-OVCSGSRATTENSHTQAYACWKHCHGFEDEVYNP
 (6184) VGREVVCNVCTKRATCFNSRTGYYGCWRHNSVSCDYLYNP
 (155) IGPERTCGLCDKRATCFNSRTGYYGCWRHNSVGFEDYLYNP
 (6280) IGREISCCNVCTKRATCFNSRTGYYACWRHNSVGFEDYLYNP

FIGURE 115 (contd.)

Section 163

(6319) 6319 6330 6340 6357

(6139) LIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTR

(5706) LIVDIQQWGYISNLQFNHDLHCNVHGHARVASVDAIMTR

(6223) LIVDIQQWGYTESLTSNHDPTCSVHKGAHVASSDAIMTR

(194) FMIDVQQWGLYC- PFRVTMTNIARYMEMHMMWASDA

(6319) LIVDIQQWGYSGSLSSNHDLHCNVHKGAVASSDAIMTR

Section 164

(6358) 6358 6370 6380 6396

(6178) CLAVYDCEFCNNENWNVEYPIISNELSENTSCRVLQRVML

(5745) CLAVENNAECQDVNWDLTYPHLANEDEVNSSCRYLQRMYL

(6262) CLAVHDCFCRSVNNWLEYPPIISNEVSVNTSCRLLQRVMF

(229) -----

(6358) CLAVHDCFCN VNNWLEYPPIISNELSVNTSCRLLQRVML

Section 165

(6397) 6397 6410 6420 6435

(6217) KAAMLCNRYTLCYDIGNPKAIACVKD--EDEFKFYDAQPI

(5784) NACVDALKVNVVYDIGNPKGIKCVRRGDVNERFYDKNPI

(6301) KAAMLCNRYDVCYDIGNPKGLACVKG--YDEFKFYDASPV

(229) -----

(6397) KAAMLCNRY VCYDIGNPKGIACVK FDEFKFYDANPI

Section 166

(6436) 6436 6450 6460 6474

(6254) VKSVKTLLEYSEEAHKDSEKDGGLCMFWNCNVDKYPNAV

(5823) VRNVKQFEYDYNQHKDKFADGLCMFWNCNVDCYPDN

(6338) VKSVKQFVYKYEAHKDQELDGLCMFWNCNVDKYPNAV

(229) -----

(6436) VKSVKQFLY YEAHKD F DGLCMFWNCNVDKYP NAV

Section 167

(6475) 6475 6480 6490 6500 6513

(6293) CRFDTRVLN LNLPGCNGGSLYVNKHAFHTKPF

(5862) CRYDTRNLSV LNLPGCNGGSLYVNKHAFHTPKFORISEP

(6377) CRFDTRVNLN LNLPGCNGGSLYVNKHAFHTSPFTRAAFE

(229) -----

(6475) CRFDTRVLN LNLPGCNGGSLYVNKHAFHT PFSRAAFE

Section 168

(6514) 6514 6520 6530 6540 6552

(6332) NLKPMPEFFYYSDTPCVYMDGMDAKQVDYVPLKSATCITR

(5901) NLKAMPEFFYYDSSPCETHLV DG-VAQDLVSLATKDCITR

(6416) NLKPMPEFFYYSDTPCVYMEGMESKQVDYVPLRSATCITR

(229) -----

(6514) NLKPMPEFFYYSDTPCVYMDGMDAKQVDYVPLKSATCITR

FIGURE 115 (contd.)

Section 169				
(6553)	6553	6560	6570	6580 6591
(6371)	CNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFD			
(5939)	CNLGGAVCKKHAQMYAEVTSYNAAVTAGFTFWVTNKLH			
(6455)	CNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFD			
(229)	-----			
(6553)	CNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFD			
Section 170				
(6592)	6592	6600	6610	6620 6630
(6410)	FYNLWNTFTKLOSLENVVYNLVKTGHYTGQAGEMPCATL			
(5978)	PYNLWKSEFALOSTDNTAYNMYKGGHYDAIAGEMPTVIT			
(6494)	FYNLWNTFTRLQSLENVVYNLVNAGHEDGRAGELPCAVT			
(229)	-----			
(6592)	FYNLWNTFTKLOSLENVVYNLVKAGHYDG AGEMPCATL			
Section 171				
(6631)	6631	6640	6650	6669
(6449)	NDKVYAKIDKEDVVFINTTPTNVAVELFAKRSIRHH			
(6017)	GDKVFIIDQVEKAVEFNQTTLPTSVAFELYAKRNIRTL			
(6533)	GEKVFAKIQNEDEVVFEKNNTTPTNVAVELFAKRSIRPH			
(229)	-----			
(6631)	GDKVIAKIQ EDVVVFINTTPTNVAVELFAKRSIR H			
Section 172				
(6670)	6670	6680	6690	6708
(6488)	PELKLFRNLNIDVCWKHVWIDYARESTFCSNTYGVCMYT			
(6056)	PNNRLKGLGVDTNGFVWIDYANCTPLYNRTVKVCAYT			
(6572)	PELKLFRNLNIDVCWSHVLWDYAKDSVFCSSYKVKCYT			
(229)	-----			
(6670)	PELKLFRNLNIDVCW HVIWDYAKDSIFCSNTYKVC YT			
Section 173				
(6709)	6709	6720	6730	6747
(6527)	DLKFIDKLNVLFDGRDNGALEAEKRSNNGVYISTTKMKS			
(6095)	DLEPNG--LVVLYDDRYG DYQSELAADNAVLYSTQCYKR			
(6611)	DLQCTESLNVLFEDGRDNGALEAEKRCRNGVYINTTKIKS			
(229)	-----			
(6709)	DL ID LNVLFEDGRDNGALEAFKKA NGVYISTTKIKS			
Section 174				
(6748)	6748	6760	6770	6786
(6566)	LSMIKGPRAELNGVVVDKVGDTDCVFFFAVRKEGODVI			
(6132)	YSYMEIPSNLLVONGMPLKDG-----ANLYV			
(6650)	LSMIKGPORADLNGVVVEKVGDSDFEFAVRKDGNDVI			
(229)	-----			
(6748)	LSMIKGP RADLNGVVVDKVGDSDFEFAVRKDGNDVI			

SEQ ID NO: 10068

SEQ ID NO: 10069

SEQ ID NO: 10070

SEQ ID NO: 9997/98

SEQ ID NO: 10071

SEQ ID NO: 10068

SEQ ID NO: 10069

SEQ ID NO: 10070

SEQ ID NO: 9997/98

SEQ ID NO: 10071

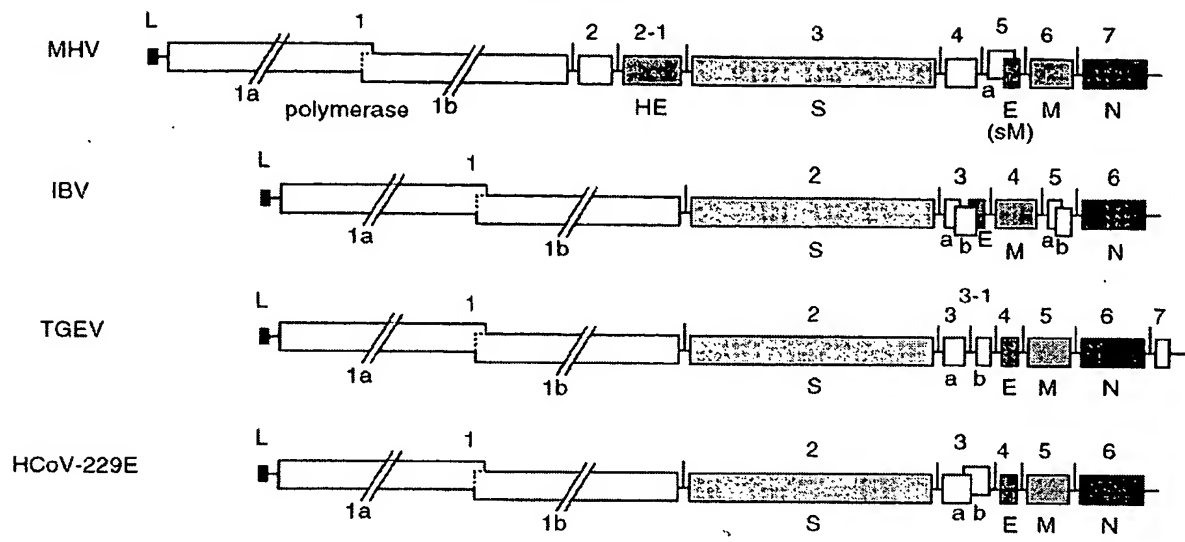
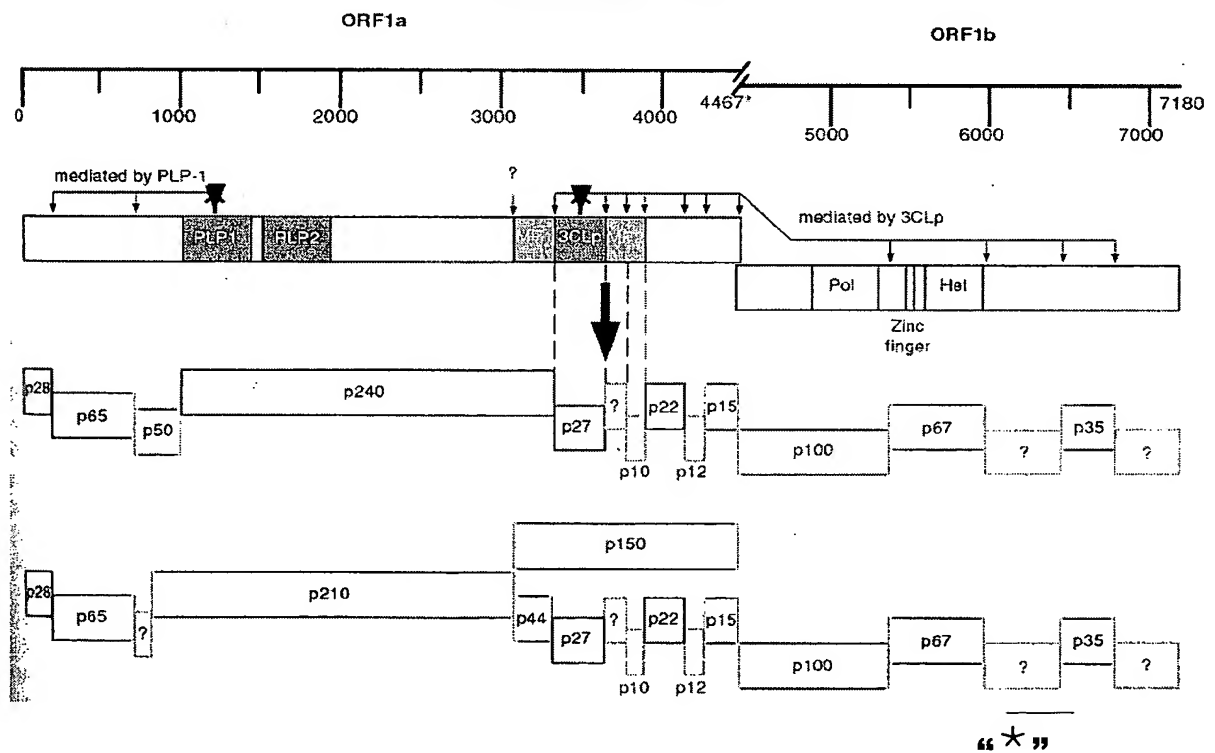
FIGURE 116**FIGURE 117**

FIGURE 118

Section 1					
(1)	1	10	20	30	40
(1)	-	GGGLPRTI	UNKKESEV	IPAYAVIT	KADAATYKVNDEL
(1)	CSTNLF	KDCSKSYSGYHP	PAHAPSE	FLAVDDKYKATG	DLAVGLDGD-KGHDL
(1)	CSTNLF	KDCSKSYSGYHP	PAHAPSE	FLAVDDKYKVG	GDLAVCLNVAD-KGHDL
(1)	CSTNLF	KDCSKSYSGYHP	PAHAPSE	FLAVDDKYKVG	GDLAVCLNVAD-KGHDL
(1)	CSTNLF	KDCSKSYSGYHP	PAHAPSE	FLAVDDKYKVG	GDLAVCLNVAD-KGHDL
Section 2					
(52)	52	60	70	80	90
(51)	RRLISM	MGFKMNYQVNGY	PNMFITREEA	IRHVRAWIG	EDVEGCHATRDAVG
(51)	RRLISM	MGFKMNYQVNGY	PNMFITREEA	IRHVRAWIG	EDVEGCHATRDAVG
(51)	RRLISM	MGFKMNYQVNGY	PNMFITREEA	IRHVRAWIG	EDVEGCHATRDAVG
(51)	RRLISM	MGFKMNYQVNGY	PNMFITREEA	IRHVRAWIG	EDVEGCHATRDAVG
(52)	RRLISM	MGFKMNYQVNGY	PNMFITREEA	IRHVRAWIG	EDVEGCHATRDAVG
Section 3					
(103)	103	110	120	130	140
(102)	TNLPLQ	LGFSTGVNLVAVPT	GYVDTENNTK	ETRVNAQTST	SEQFKHLIPLM
(102)	TNLPLQ	LGFSTGVNLVAVPT	GYVDTENNTK	ETRVNAQTST	SEQFKHLIPLM
(102)	TNLPLQ	LGFSTGVNLVAVPT	GYVDTENNTK	ETRVNAQTST	SEQFKHLIPLM
(102)	TNLPLQ	LGFSTGVNLVAVPT	GYVDTENNTK	ETRVNAQTST	SEQFKHLIPLM
(103)	TNLPLQ	LGFSTGVNLVAVPT	GYVDTENNTK	ETRVNAQTST	SEQFKHLIPLM
Section 4					
(154)	154	160	170	180	190
(153)	YKGLP	WNVVR	IKIVQMLSDTL	KGLSDRVV	FVLWAHGFELTSMKYFVKIGPE
(153)	YKGLP	WNVVR	IKIVQMLSDTL	KGLSDRVV	FVLWAHGFELTSMKYFVKIGPE
(153)	YKGLP	WNVVR	IKIVQMLSDTL	KGLSDRVV	FVLWAHGFELTSMKYFVKIGPE
(153)	YKGLP	WNVVR	IKIVQMLSDTL	KGLSDRVV	FVLWAHGFELTSMKYFVKIGPE
(154)	YKGLP	WNVVR	IKIVQMLSDTL	KGLSDRVV	FVLWAHGFELTSMKYFVKIGPE
Section 5					
(205)	205	210	220	230	240
(204)	RTCC	LCDKRATCFSTSS	SDTYACWNH	SVGFDYVYNPF	MIDVQQWGLYGSLQF
(204)	RTCC	LCDKRATCFSTSS	SDTYACWNH	SVGFDYVYNPF	MIDVQQWGLYGSLSS
(204)	RTCC	LCDKRATCFSTSS	SDTYACWNH	SVGFDYVYNPF	MIDVQQWGLYGSLTS
(204)	RTCC	LCDKRATCFSTSS	SDTYACWNH	SVGFDYVYNPF	MIDVQQWGLYGSLSS
(205)	RTCC	LCDKRATCFSTSS	SDTYACWNH	SVGFDYVYNPF	MIDVQQWGLYGSLSS
Section 6					
(256)	256	270	280	290	306
(255)	NHDLHC	SVHKG	AHVASSDAIMTR	CLAVHDCFCNSV	NWNLEYPIISNELSVN
(255)	NHDLHC	SVHKG	AHVASSDAIMTR	CLAVHDCFCNSV	NWNLEYPIISNELSVN
(255)	NHDLHC	SVHKG	AHVASSDAIMTR	CLAVHDCFCNSV	NWNLEYPIISNELSVN
(255)	NHDLHC	SVHKG	AHVASSDAIMTR	CLAVHDCFCNSV	NWNLEYPIISNELSVN
(256)	NHDLHC	SVHKG	AHVASSDAIMTR	CLAVHDCFCNSV	NWNLEYPIISNELSVN

FIGURE 118 (contd.)

Section 7

(307) 307	320	330	340	357
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(306) SSCRYLQRMVNLNACMDALKVNVVYDIGNPKGIKCVRRGQDVNFRFYDKNPIV
 (306) TSCDVLQRVMLKAAMLCNRYTTCYDIGNPKAIACVK--DFDEKIFYDAQEIV
 (306) TSCDVLQRVMLKAAMLCNRYDVCYDIGNPKGIACVK--GYDEKIFYDASPIV
 (306) TSCDVLQRVMLKAAMLCNRYTVGYDIGNPKGIACVK--DFDEKIFYDANPIV
 (307) TSCRLQLRVMLKAAMLCNRYTVGYDIGNPKGIACVK DFDEKIFYDANPIV

Section 8

(358) 358	370	380	390	408
-----------	-----	-----	-----	-----

(357) RNVKOEEDYNQHKDKADGLCMFWNCNVDCYFDNSLVCRMDTRNL SVFNL
 (355) KSVKTLTLYSFEAHKDSFKDGLCMFWNCNVDKYPANAVVCRFDTRVLNNL
 (355) KSVKOEELYSYEAHKDQELDGLCMFWNCNVDKYPANAVVCRFDTRVLNKLNL
 (355) KSVKOEELYSYEAHKDSFKDGLCMFWNCNVDKYPANAVVCRFDTRVLN-LNL
 (358) KSVKQFLYSYEAHKDSFKDGLCMFWNCNVDKYPANAVVCRFDTRVLN LNL

Section 9

(409) 409	420	430	440	459
-----------	-----	-----	-----	-----

(408) PGCNGGSLYVNHAFYCPKPIRISFRNLKAMPFFEDSSPCETIQ-VDGVA
 (406) PGCNGGSLYVNHAFHFKPESRAAFENLKMPFFFYYSDFPCVYMDGMDAKQ
 (406) PGCNGGSLYVNHAFHFKPESRAAFENLKMPFFFYYSDFPCVYMDGMDAKQ
 (405) PGCNGGSLYVNHAFHFKPESRAAFENLKMPFFFYYSDFPCVYMDGMDAKQ
 (409) PGCNGGSLYVNHAFHFKPESRAAFENLKMPFFFYYSDFPCVYMDGMDAKQ

Section 10

(460) 460	470	480	490	500	510
-----------	-----	-----	-----	-----	-----

(458) QDLVSLATKDCITRCNLGGAVCKKHAAEYREYLESYNTATTAGFTFWVYKT
 (457) VDYVPLKSATCITRCNLGGAVCKKHAAEYREYLESYNTATTAGFTFWVYKT
 (457) VDYVPLKSATCITRCNLGGAVCKKHAAEYREYLESYNTATTAGFTFWVYKT
 (456) VDYVPLKSATCITRCNLGGAVCKKHAAEYREYLESYNTATTAGFTFWVYKT
 (460) VDYVPLKSATCITRCNLGGAVCKKHAAEYREYLESYNTATTAGFTFWVYKT

Section 11

(511) 511	524	
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(509) LNPYNLWNTFTKLQ SEQ ID NO: 10073
 (508) FDEYNLWNTFTKLQ SEQ ID NO: 10074
 (508) FDEYNLWNTFTKLQ SEQ ID NO: 10075
 (507) FDEYNLWNTFTKLQ SEQ ID NO: 10076
 (511) FDEYNLWNTFTKLQ SEQ ID NO: 10077

FIGURE 119

tagtcaaaacccacagaatgattccagcaggcataagtatctgatgaagtagaaaagcaa
 - - - V S D E V E K Q
 gttgcacgt**TTG**tcacacagacaacacgttctttcaggtccaatc**TTG**acaaagtacttc
 V A R L S H R Q H V L S G P I L T K Y F
 attgatgtaagctcaaagccatgCGCCCAAAGGACGAACACGACTCTGTCTGACAATCCT
 I D V S S K P C A Q R T N T T L S D N P
 ttcagtgtatcactgagcatttgtactatcttaatacgactacattccagggcaagcct
 F S V S L S I C T I L I R T T F Q G K P
 ttatac**ATG**agtggtataagatgtttaaactgctcactgggtggaggtttgtgcattaact
 L Y M S G I R C L N C S L V E V C A L T
 Ctggtgaattttgtgttattttcagtggtcaacataa **SEQ ID NO: 10080**
 L V N F V L F S V S T - **SEQ ID NO: 10027**

FIGURE 120**FIGURE 120A**

PRHTQRT-PTVDSSL-WVSK-ITKSMVTLICLSPAKKLFVTFVRGLALM-RAVMQL
 EMLWVLTYLSS-DFLQVLT--LYRLVMLTLKITQNSPELMQNLHQVTSNLILYHSC
 IKACPGM-CVLR-YKCSVIH-KDCQTESCSSFGRMALSLHQ-STLSRLDLKERVVC
 VTNVQLAFLHQLMPAGIILWVLTMSITHL-LMFSSGALRVTFRVMTNRIARYME
 MHMWLVVMLS-LDV-QSMSALLSALIGLLNTLL-EMN-GLILLAKEYNTWL-SLHC
 LLISFQFFMT-EIQRLSSVCLRLK-NGSSTMLSHVVTCLTK-RNSSILMLYITINS
 LMFVFCFGIVTLIVTQPMQLCVGLTQESCQT-TYQAVMVVVC-ISMHSTLQLSIK
 VHLLI-SNCLSFTILIVLVSLMANK-CRILIMFHSNLLRVLHDAI-VVLFADTMQM
 STDSTWMHII--FLDLAYGFTNNLILITCGIHLPGYRV

FIGURE 120B

LGIPKGHDLP-THLYDGFQNELPSQWLP-YVYHPRRSYSSRSCVDWL-CRGLSCN-
 RCCGY-PTSPARIFYRC-LSSCTDWLC-H-K-HRIHQS-CKTSTR-PV-TSYTTHV
 -RLALECSAY-DSTNAQ-YTERIVRQSRVRPLGAWL-AYINEVLCQDWT-KNVLSV
 -QTCNLLFYFIRYLCLLESFCGF-LCL-PIYD-CSAVGLYG-PSE-P-PTLPGTWK
 CTCG-L-CYHD-MFSSP-VLC-AR-LVC-IPYYRR-TEG-FCLQKSTTHGCEVCIA
 C--VSSSS-HRKSKGYQVCASG-SRMEVLRCSAM--QSLQNRGTLLFLCYTSR-IH
 -WCLFVLEL-R-SLPSQCNCV-V-HKSLVKLELTRL-WW-FVCE-ACIPHSSFR-K
 CIY-FKAI AFLLLF--SL-VSWQTSSVGY-LCSTQICYVYYTMQFRWCCLQTPCK-
 VPTVLGCI-YDDFCWI-PMDLQTI-YL-PVEYIYQVTEF

FIGURE 120C

-AYPKDMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAV
 GTNLPLQLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWN
 VVRIKIVQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFST
 SSDTYACWNHSGFDYVYNPFMIDVQQWGFSTGNLQSNHDQHCQVHGNAHVASCDAIMTR
 CLAVHECFVKRVDWSVEYPIIGDELRVNSACRKYQHMVVKSAALLADKFPVLHDIGNPKA
 IKCVPQAEVEWKFYDAQPCSDKAYKIEELFYSYAIHHDKFTDGVCLFWNCNVDRYPANA
 IVCRFDTRVLSNLNLPDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESH
 GKQVVSIDIDYVPLKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQF
 DTYNLWNTFTRLQSL

FIGURE 120D

-TL-PGKCIPQVISIKLFVNP-AKSSRNHHIICIQVLSVLICMVSANSTT-IASCNTRS
 RFEWNIINIRHYLFAMRLTRTIRIVKERQLL-ISKCTFIESWSVECLMIIHIQTITITAW
 -VQV-QDSCVKPTHNCIGWVTINVTIPKQNTISEFIVMYSIRIEEFLYFVSFVTTWLS
 IVELPFYFSLRHTLDSLWISYVMKNWKLISKQCRLHNHVLYFSASRINPQFISYNRVFN
 RPINALNKALMDC-TSSHDSITTSHMCISMYLAMLVMVTLKVTRKAPLLNINHKWVIDI
 VKTHRMIPAGISI--SRKASCTFVTQTTRSFRSNLDKVLH-CKLKAMRPKDEHDSV-QS
 FQCITEHLYLNTHYIPGQAFIHEWYKMFKLVTWWRFCINSGEFCVIFSUNITSRYSY-
 VNTCRKS-LER-VSTHSISSCMTALYIKANPRTNVTNSFFAGDKHIRVTIDLVIHFETH
 HRDESTVGHVLWVCL

FIGURE 120E

KLCNLVNVFHLR-VSNCL-IHRLNPAEIIILYASKYCRYSAWCLQTAPPKLHRVIHVA
 DLSGT-SISDTTCLP-DSQGLSE--KKGNCFKLVNALLSKAGVWNAFLTYKLPPSQPG
 KFKFDKTLVSNLHTIALAG-RSTLQFQNKQTPSVNLS-CIA-E-KSSSIL-ALSLHG-A
 S-NFHSTSA-GTHLIAFGFPMS-RTGNLSASNADFTTMCCTFLQAEFLTSSSPIIGYST
 DQSTRLTKHSWTAKHLVMIASQLATCAFPCTWQCWSWLL-RLPVKPHC-TSIINGL-T-
 SKPTE-FQQA-VSDEVEKQVARLSHRQHVLSPILTKYFIDVSSKPCAQRTNTTSLSDNP
 FSVSLSICTILIRTTFQGKPLYMSGIRCLNWSPGGGFALTLVNSVLFSVST-PVGTATK
 LTPVENPSWRGRLVPTASLVA-QPSTSKPIHART-RIASSRVINILG-PLTW-FILKPI
 IEMSLR-VMSFGYA-

FIGURE 120F

NSVTW-MYSTGYKYQIVCKSIG-IQQKSSYYMHPSTVGTHLHGVCKQHHLNCIV-YT-Q
 I-VEHNQYPTLLVCHETHKDYQNSKRKAIALN--MHFYRKLECGMHAYSHTNYHHHSLV
 SSSLTRLLCQTYTQLHWLGNDQRYNSKTNKHHQ-IYRDV-HKNRRVPLFCKLCHYMAEH
 RRTSILLQPEAHT--PLDFLCHEELETYQQAMQTSQPCVVLFCKQN-PSVHLL--GIIQQ
 TNQRA-QSTHGLLNI-S--HHN-PHVHFPVPGNVGHGYSEGYP-SPTAEHQS-MGYRHS
 QNPQNDSSSRHKYLMK-KSKLHVCHTDNTFFQVQS-QSTSLM-AQSHAPKGRTRLCLTIL
 SVYH-AFVLS-YALHSRASLYT-VV-DV-TGHLVEVLH-LW-ILCYFQCQHNQSVQLLS
 -HL-KILAGEVG-YPQHL-LHDSPLHQSQSTHERDE-LLRG--TY-GNH-LGNSF-NPS
 -R-VYGRSCPLGMPR

FIGURE 121

	10	20	30	40	50	60
SEQ ID NO:10033	-----TACCGTAGACTCATCTCTATGATGGGTTTCAAAA					
SEQ ID NO:10084	CCTAGGCATACCCAAAGGACATGACCTACCGTAGACTCATCTCTATGATGGGTTTCAAAA					
Consensus	TACCGTAGACTCATCTCTATGATGGGTTTCAAAA					
Prim. cons.	CCTAGGCATACCCAAAGGACATGACCTACCGTAGACTCATCTCTATGATGGGTTTCAAAA					

	70	80	90	100	110	120
SEQ ID NO:10033	TGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAAGAAGCTATTTCGTC					
SEQ ID NO:10084	TGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAAGAAGCTATTTCGTC					
Consensus	TGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAAGAAGCTATTTCGTC					
Prim. cons.	TGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCCGCGAAGAAGCTATTTCGTC					

	130	140	150	160	170	180
SEQ ID NO:10033	ACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAGAGATGCTGTGG					
SEQ ID NO:10084	ACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAGAGATGCTGTGG					
Consensus	ACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAGAGATGCTGTGG					
Prim. cons.	ACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATGCAACTAGAGATGCTGTGG					

	190	200	210	220	230	240
SEQ ID NO:10033	GTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA					
SEQ ID NO:10084	GTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA					
Consensus	GTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA					
Prim. cons.	GTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA					

	250	260	270	280	290	300
SEQ ID NO:10033	CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCAC					
SEQ ID NO:10084	CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCAC					
Consensus	CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCAC					
Prim. cons.	CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCAC					

	310	320	330	340	350	360
SEQ ID NO:10033	CAGGTGACCAGTTTAAACATCTTATACC-----					
SEQ ID NO:10084	CAGGTGACCAGTTTAAACATCTTATACCACTCATGTATAAAGGCTTGCCCTGGAATGTAG					
Consensus	CAGGTGACCAGTTTAAACATCTTATACC					
Prim. cons.	CAGGTGACCAGTTTAAACATCTTATACCACTCATGTATAAAGGCTTGCCCTGGAATGTAG					

etc.

FIGURE 122**5'3' Frame 1**

cctaggcatacccaaaggacatgacctaccgtagactcatctctatgatggggtttcaaaa
P R H T Q R T - P T V D S S L - W V S K
tgaattaccaagtcaatgggttacctaataatgtttatcacccgcgaagaagctattcgtc
- I T K S M V T L I C L S P A K K L F V
acgttcgtgcgtggattggcctttgatgtagagggtgtcatgcaactagagatgctgtgg
T F V R G L A L M - R A V M Q L E M L W
gtactaacctacctctccagctaggattttctacagggtgttaacttagtagctgtaccga
V L T Y L S S - D F L Q V L T - - L Y R
ctgggttatgttgacactgaaaataaacacagaattcaccagagttaatgcaaacctccac
L V M L T L K I T Q N S P E L M Q N L H
cagggtgaccagtttaaacatcttataaccactcatgtataaaggcttgccctggaatgtag
Q V T S L N I L Y H S C I K A C P G M -
tgcgtattaagatagtacaaatgctcagtgatacactgaaaggattgtcagacagagtcg
C V L R - Y K C S V I H - K D C Q T E S
tgttcgtcctttgggcgcgtggcctttgagcttacatcaatgaagtactttgtcaagattg
C S S F G R M A L S L H Q - S T L S R L
gacctgaaagaacgtgttgctgtgtgacaaacgtgcaacttgcttttctacttcatcag
D L K E R V V C V T N V Q L A F L L H Q
atacttatgcctgctggaatcattctgtgggttttgactatgtctataacccatttatga
I L M P A G I I L W V L T M S I T H L -
ttgatgttcagcagtggggcctttacgggtaaccttcagagtaaccatgaccaacattgcc
L M F S S G A L R V T F R V T M T N I A
aggtacatggaaatgcacatgtggcctagttgtgatgctatcatgactagatgttttagcag
R Y M E M H M W L V V M L S - L D V - Q
tccatgagtgctttgttaagcgcgttgattggctgttggaataccctattataggagatg
S M S A L L S A L I G L L N T L L - E M
aactgagggttaattctgcttgcaaaaagtacaacacatgggtgtggaagtctgcattgc
N - G L I L L A E K Y N T W L - S L H C
ttgctgataagtttccagttcttcatgacataggaaatccaaaggctatcaagtgtgtgc
L L I S F Q F F M T - E I Q R L S S V C
ctcaggctgaagtagaatggaagttctacgatgctcagccatgtagtgacaaagcttaca
L R L K - N G S S T M L S H V V T K L T
aaatagaggaactcttctatttcttatgctatacatcacgataaattcactgatgggtgttt
K - R N S S I L M L Y I T I N S L M V F
gtttgttttgggaattgtaacgttgatcggttaccagccaatgcaattgtgtgtaggtttg
V C F G I V T L I V T Q P M Q L C V G L
acacaagagtcttgtcaaacttgaacttaccaggctgtgatggtaggtgtgtatgtga
T Q E S C Q T - T Y Q A V M V V V C M -
ataagcatgcattccacactccagctttcgataaaagtgcatttactaatttaaagcaat
I S M H S T L Q L S I K V H L L I - S N
tgccttttcttttactattctgatagtccttgtgagtcctcatggcaacaagtagtgctgg
C L S F T I L I V L V S L M A N K - C R
atattgattatgttccactcaaactctgctacgtgtattacacgatgcaatttaggtgggtg
I L I M F H S N L L R V L H D A I - V V
ctgttttgagacacccatgcaaatgagtagcagtagtcttggtatgcataataatgatga
L F A D T M Q M S T D S T W M H I I - -
tttctgctggatttagcctatggattttacaacaatttgataacttataacctgtggaata
F L L D L A Y G F T N N L I L I T C G I

catttaccaggttacagagttta
H L P G Y R V

5'3' Frame 2

cctaggcatacccaaaggacatgacctaccgtagactcatctctatgatggggtttcaaaat
L G I P K G H D L P - T H L Y D G F Q N
gaattaccaagtcaatgggttaccctaatatgtttatcacccgcgaagaagctattcgta
E L P S Q W L P - Y V Y H P R R S Y S S
cgttcgtgctggattggccttgatgtagagggctgtcatgcaactagagatgctgtggg
R S C V D W L - C R G L S C N - R C C G
tactaacctacctctccagctaggatgtttctacaggtgttaacttagtagctgtaccgac
Y - P T S P A R I F Y R C - L S S C T D
tggttatgttgacactgaaaataacacagaattcaccagaggttaatgcaaaacctccacc
W L C - H - K - H R I H Q S - C K T S T
aggtgaccagtttaaacatcttataaccactcatgtataaaggcttgccctggaatgtagt
R - P V - T S Y T T H V - R L A L E C S
gcgatattaagatagtacaaatgctcagtgatacactgaaaggattgtcagacagagtcgt
A Y - D S T N A Q - Y T E R I V R Q S R
gttcgtcctttgggcgcagtggttgagcttacatcaatgaagtactttgtcaagattgg
V R P L G A W L - A Y I N E V L C Q D W
acctgaaagaacgtgttgctgtgtgacaaacgtgcaacttgcttttctacttcatcaga
T - K N V L S V - Q T C N L L F Y F I R
tacttatgcctgctggaatcattctgtgggttttgactatgtctataacccatttatgat
Y L C L L E S F C G F - L C L - P I Y D
tgatgttcagcagtggtggcctttacgggtaaccttcagagtaaccatgaccaacattgcc
- C S A V G L Y G - P S E - P - P T L P
ggtacatggaaatgcacatgtggctagtgtgtgatgctatcatgactagatgttttagcagt
G T W K C T C G - L - C Y H D - M F S S
ccatgagtgctttgttaagcgcgttgattggtctgttgaaataccctattataggagatga
P - V L C - A R - L V C - I P Y R R -
actgagggttaattctgcttgagaaaaagtacaacacatgggttggaagtctgcattgct
T E G - F C L Q K S T T H G C E V C I A
tgctgataagtttccagttcttcatgacataggaaatccaaaggctatcaagtgtgtgcc
C - - V S S S - H R K S K G Y Q V C A
tcaggctgaagtagaatggaagtctacgatgctcagccatgtagtgacaaagcttaca
S G - S R M E V L R C S A M - - Q S L Q
aatagaggaactcttctattcttatgctatacatcacgataaattcactgatgggtgttg
N R G T L L F L C Y T S R - I H - W C L
tttggtttggaattgtaacgcttgatcggttaccagccaatgcaattgtgtgtgaggtttga
F V L E L - R - S L P S Q C N C V - V -
cacaagagtcctgtcaaaccttgaacttaccaggctgtgatgggtgtagtttgatgtgaa
H K S L V K L E L T R L - W W - F V C E
taagcatgcattccacactccagctttcgataaaagtgcatttactaatttaaagcaatt
- A C I P H S S F R - K C I Y - F K A I
gcctttcttttactattctgatagtccttgtagtctcatggcaacaagtagtgtcgga
A F L L L F - - S L - V S W Q T S S V G
tattgattatgttccactcaaactctgctacgtgtattacacgatgcaatttaggtggtgc
Y - L C S T Q I C Y V Y Y T M Q F R W C
tggttgagacacatgcaaatgagtagcagcagcttggatgcatataatatgatgat

C L Q T P C K - V P T V L G C I - Y D D
 ttctgctggatttagcctatggatttacaaacaatttgatacttataacctgtggaatac
 F C W I - P M D L Q T I - Y L - P V E Y
 atttaccagggttacagagttta
 I Y Q V T E F

5'3' Frame 3

cctaggcatacccaaaggacATGacctaccgtagactcatctctatgatgggtttcaaaatg
 - A Y P K D M T Y R R L I S M M G F K M
 aattaccaagtcaatggttaccctaataatgtttatcacccgcgaagaagctattcgtcac
 N Y Q V N G Y P N M F I T R E E A I R H
 gttcgtgctggattggctttgatgtagagggtgtcatgcaactagagatgctgtgggt
 V R A W I G F D V E G C H A T R D A V G
 actaacctacctctccagctaggattttctacagggtgttaacttagtagctgtaccgact
 T N L P L Q L G F S T G V N L V A V P T
 gggtatgttgacactgaaaataacacagaattcaccagagttaatgcaaaacctccacca
 G Y V D T E N N T E F T R V N A K P P P
 ggtgaccagtttaaacatcttataccactcatgtataaaggcttgccctggaatgtagt
 G D Q F K H L I P L M Y K G L P W N V V
 cgtattaagatagtacaaatgctcagtgatacactgaaaggattgtcagacagagtcgtg
 R I K I V Q M L S D T L K G L S D R V V
 ttcgtcctttgggcgcagtggtttgagcttacatcaatgaagtactttgtcaagattgga
 F V L W A H G F E L T S M K Y F V K I G
 cctgaaagaacgtgttgtctgtgtgacaaacgtgcaacttgcttttctacttcatcagat
 P E R T C C L C D K R A T C F S T S S D
 acttatgcctgctggaatcattctgtgggttttgactatgtctataaccatttatgatt
 T Y A C W N H S V G F D Y V Y N P F M I
 gatgttcagcagtggtgggtttacgggtaaccttcagagtaaccatgaccaacattgccag
 D V Q Q W G F T G N L Q S N H D Q H C Q
 gtacatggaaatgcacatgtggctagtgtgtatcatgactagatgttttagcagtc
 V H G N A H V A S C D A I M T R C L A V
 catgagtgctttgttaagcgcgttgattggtctgttgaaataccctattataggagatgaa
 H E C F V K R V D W S V E Y P I I G D E
 ctgagggttaattctgtctgcagaaaagtacaacacatgggttggaagtctgcattgctt
 L R V N S A C R K V Q H M V V K S A L L
 gctgataagtttccagttcttcatgacataggaaatccaaaggctatcaagtgtgtgcct
 A D K F P V L H D I G N P K A I K C V P
 caggctgaagtagaatggaagtctacgatgctcagccatgtagtgacaaagcttacaaa
 Q A E V E W K F Y D A Q P C S D K A Y K
 atagaggaactcttctattcttatgctatacatcacgataaattcactgatgggtgtttgt
 I E E L F Y S Y A I H H D K F T D G V C
 ttgttttggaattgtaacgttgatcggttaccagccaatgcaattgtgtgtaggtttgac
 L F W N C N V D R Y P A N A I V C R F D
 acaagagtcttgtcaaacttgaacttaccaggctgtgatgggtgtagttttgtatgtgaat
 T R V L S N L N L P G C D G G S L Y V N
 aagcatgcattccacactccagctttcgataaaagtgcatttactaatttaaagcaattg
 K H A F H T P A F D K S A F T N L K Q L
 cctttcttttactattctgatagtccttgtgagtcctcatggcaacaagtagtgcggat
 P F F Y Y S D S P C E S H G K Q V V S D

attgattatgttccactcaaattctgctacgtgtattacacgatgcaatttaggtggtgct
I D Y V P L K S A T C I T R C N L G G A
gtttgcagacaccatgcaaattgagtaccgacagtacttggatgcatataatatgatgatt
V C R H H A N E Y R Q Y L D A Y N M M I
tctgctggatttagcctatggatttacaacaatttgatacttataacctgtggaataca
S A G F S L W I Y K Q F D T Y N L W N T
tttaccaggttacagagttta
F T R L Q S L

3'5' Frame 1

taaactctgtaacctggtaaattgtattccacaggttataagtatcaaattgtttgtaaatt
- T L - P G K C I P Q V I S I K L F V N
ccataggctaaatccagcagaaatcatcatatttatatgcatccaagtactgtcggctactc
P - A K S S R N H H I I C I Q V L S V L
atttgcacatgggtgtctgcaaacagcaccacctaattgcatcgtgtaatacacgtagcaga
I C M V S A N S T T - I A S C N T R S R
tttgagtggaaacataatcaataatccgacactacttgtttgcatgagactcacaaggact
F E W N I I N I R H Y L F A M R L T R T
atcagaatagtaaaagaaaggcaattgcttttaattagtaaatgcacttttatcgaaagc
I R I V K E R Q L L - I S K C T F I E S
tggagtgtggaatgcatgcttattcacatacaaactaccaccatcacagcctggtaagtt
W S V E C M L I H I Q T T T I T A W - V
caagtttgacaagactccttgtgtcaaacctacacacaattgcattggctgggtaacgatc
Q V - Q D S C V K P T H N C I G W V T I
aacgttacaattccaaaacaaacaaacaccatcagtggaatttatcgtgatgtatagcata
N V T I P K Q T N T I S E F I V M Y S I
agaatagaagagttccttctattttgtaagctttgtcactacatggctgagcatcgtagaa
R I E E F L Y F V S F V T T W L S I V E
cttccatttctacttcagcctgaggcacacacttgatagcctttggatttcttatgtcatg
L P F Y F S L R H T L D S L W I S Y V M
aagaactggaaacttatcagcaagcaatgcagacttcacaaccatgtgttgacttttct
K N W K L I S K Q C R L H N H V L Y F S
gcaagcagaattaacctcagttcatctcctataatagggatttcaacagaccaatcaac
A S R I N P Q F I S Y N R V F N R P I N
gcgcttaacaaagcactcatggactgctaaccatctagtcatgatagcatcacaactagc
A L N K A L M D C - T S S H D S I T T S
cacatgtgcatttccatgtacctggcaatgttggtcatgggttactctgaagggttaccggt
H M C I S M Y L A M L V M V T L K V T R
aaagccccactgctgaacatcaatcataaattgggttatagacatagtcaaaacccacaga
K A P L L N I N H K W V I D I V K T H R
atgattccagcaggcataagtatctgatgaagtagaaaagcaagttgcacgtttgtcaca
M I P A G I S I - - S R K A S C T F V T
cagacaacacgttctttcaggtccaatcttgacaaagtaacttcattgatgtaagctcaa
Q T T R S F R S N L D K V L H - C K L K
gcatgtgcgccccaaaggacgaacacgactctgtctgacaatcctttcagtgatcactgag
A M R P K D E H D S V - Q S F Q C I T E
catttgactatcttaatacgcactacattccagggcaagcctttatacatgagtggtat
H L Y Y L N T H Y I P G Q A F I H E W Y
aagatgtttaaactgggtcacctgggtggaggttttgcattaactctggtgaattctgtgtt

K M F K L V T W W R F C I N S G E F C V
 attttcagtggtcaacataaccagtcggtacagctactaagttaacacctgtagaaaatcc
 I F S V N I T S R Y S Y - V N T C R K S
 tagctggagaggttaggttagtaccacagcatctctagttgcatgacagccctctacatc
 - L E R - V S T H S I S S C M T A L Y I
 aaagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacatattagg
 K A N P R T N V T N S F F A G D K H I R
 gtaaccattgacttggttaattcattttgaaacccatcatagagatgagtcctacggtaggt
 V T I D L V I H F E T H H R D E S T V G
 catgtcctttgggtatgcctagg
 H V L W V C L

3'5' Frame 2

taaactctgtaacctggttaaattgtattccacaggttataagtatcaaattgtttgtaaattc
 K L C N L V N V F H R L - V S N C L - I
 cataggctaaatccagcagaaatcatcatattatgcatccaagtactgtcgggtactca
 H R L N P A E I I I L Y A S K Y C R Y S
 tttgcatggtgtctgcaaacagcaccacctaattgcatcgtgtaatacacgtagcagat
 F A W C L Q T A P P K L H R V I H V A D
 ttgagtggaaacataatcaatatccgacactacttgtttgccatgagactcacaaggacta
 L S G T - S I S D T T C L P - D S Q G L
 tcagaatagtaaaagaaaggcaattgcttttaaattagtaaatgcacttttatcgaaagct
 S E - - K K G N C F K L V N A L L S K A
 ggagtgtggaatgcatgcttattcacatacaaactaccaccatcacagcctggttaagttc
 G V W N A C L F T Y K L P P S Q P G K F
 aagtttgacaagactcttgtgtcaaacctacacacaattgcattggctgggtaacgatca
 K F D K T L V S N L H T I A L A G - R S
 acgtttacaattccaaaacaaacaaacaccatcagtgaaatttatcgatgatagcataa
 T L Q F Q N K Q T P S V N L S - C I A -
 gaatagaagagttccttctatttttgtaagctttgtcactacatggctgagcatcgtagaac
 E - K S S S I L - A L S L H G - A S - N
 ttccattctacttcagcctgaggcacacacttgatagccttttgatttcctatgtcatga
 F H S T S A - G T H L I A F G F P M S -
 agaactggaaacttatcagcaagcaatgcagacttcacaacccatgtgttgacttttctg
 R T G N L S A S N A D F T T M C C T F L
 caagcagaattaaccctcagttcatctcctataatagggtattcaacagaccaatcaacg
 Q A E L T L S S S P I I G Y S T D Q S T
 cgcttaacaaagcactcatggactgctaaacatctagtcatgatagcatcacaactagcc
 R L T K H S W T A K H L V M I A S Q L A
 acatgtgcatttccatgtacctggcaatgttggtcatggttactctgaagggttaccgta
 T C A F P C T W Q C W S W L L - R L P V
 aagccccactgctgaacatcaatcataaatgggttatagacatagtcaaaacccacagaa
 K P H C - T S I I N G L - T - S K P T E
 tgattccagcaggcataagtatctgatgaagtagaaaagcaagttgcacgtttgtcacac
 - F Q Q A - V S D E V E K Q V A R L S H
 agacaacacggttctttcaggtccaatcttgacaaagtacttcattgatgtaagctcaaag
 R Q H V L S G P I L T K Y F I D V S S K
 ccatgcgccc aaaggacgaacacgactctgtctgacaatcctttcagtgatcactgagc
 P C A Q R T N T T L S D N P F S V S L S

atttggtactatcttaatacgcactacattccagggcaagcctttatacatgagtgggtata
 I C T I L I R T T F Q G K P L Y M S G I
 agatgttttaactgggtcacctgggtggaggttttgcattaactctgggtgaattctgtgtta
 R C L N W S P G G G F A L T L V N S V L
 ttttcagtgtcaacataaccagtcggtacagctactaagttaacacctgtagaaaatcct
 F S V S T - P V G T A T K L T P V E N P
 agctggagaggttaggttagtaccacagcatctctagttgcatgacagccctctacatca
 S W R G R L V P T A S L V A - Q P S T S
 aagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacatattaggg
 K P I H A R T - R I A S S R V I N I L G
 taaccattgacttggttaattcattttgaaacccatcatagagatgagtcctacggtaggtc
 - P L T W - F I L K P I I E M S L R - V
 atgtcctttgggtatgcctagg
 M S F G Y A -

3'5' Frame 3

taaactctgtaacctggtaaattgtattccacaggttataagtatcaaattgtttgtaaattcc
 N S V T W - M Y S T G Y K Y Q I V C K S
 ataggctaaatccagcagaaatcatcatattatatgcatccaagtactgtcgggtactcat
 I G - I Q Q K S S Y Y M H P S T V G T H
 ttgcatgggtgtctgcaaacagcaccacctaattgcatcgtgtaatacacgtagcagatt
 L H G V C K Q H H L N C I V - Y T - Q I
 tgagtggaaacataatcaatatccgacactacttgtttgccatgagactcacaaggactat
 - V E H N Q Y P T L L V C H E T H K D Y
 cagaatagtaaaagaaaggcaattgcttttaaattagtaaatgcactttttatcgaaagctg
 Q N S K R K A I A L N - - M H F Y R K L
 gagtgtggaatgcatgcttattcacatacaaaactaccaccatcacagcctggtaagttca
 E C G M H A Y S H T N Y H H S L V S S
 agtttgacaagactcttgtgtcaaacctacacacaattgcattggctgggtaacgatcaa
 S L T R L L C Q T Y T Q L H W L G N D Q
 cgttacaattccaaaacaaacaaacacatcagtggaatttatcgtgatgtatagcataag
 R Y N S K T N K H H Q - I Y R D V - H K
 aatagaagagttcctctattttgtaagctttgtcactacatggctgagcatcgtagaact
 N R R V P L F C K L C H Y M A E H R R T
 tccattctacttccagcctgaggcacacacttgatagcctttggatttcctatgtcatgaa
 S I L L Q P E A H T - - P L D F L C H E
 gaactggaaacttatcagcaagcaatgcagacttcacaaccatgtgttgacttttctgc
 E L E T Y Q Q A M Q T S Q P C V V L F C
 aagcagaattaaccctcagttcatctcctataatagggtattcaacagaccaatcaacgc
 K Q N - P S V H L L - - G I Q Q T N Q R
 gcttaacaaagcactcatggactgctaaacatctagtcatgatagcatcacactagcca
 A - Q S T H G L L N I - S - - H H N - P
 catgtgcatttccatgtacctggcaatggttgcatggttactctgaagggtaccggtaa
 H V H F H V P G N V G H G Y S E G Y P -
 agccccactgctgaacatcaatcataaatgggttatagacatagtcaaaaccacagaat
 S P T A E H Q S - M G Y R H S Q N P Q N
 gattccagcaggcataagtatctgatgaagtagaaaagcaagttgcacgtttgtcacaca
 D S S R H K Y L M K - K S K L H V C H T
 gacaacacgttcttttcaggtccaatcttgacaaagtacttcattgatgtaagctcaaagc

D N T F F Q V Q S - Q S T S L M - A Q S
catgcgccc aaaggacgaacacgactctgtctgacaatcctttcagtgtatcactgagca
H A P K G R T R L C L T I L S V Y H - A
tttgtagtactatcttaatacgcactacattccagggcaagcctttatacatgagtggtataa
F V L S - Y A L H S R A S L Y T - V V -
gatgttttaaactggtcacctgggtggaggttttgcattaactctgggtgaattctgtgttat
D V - T G H L V E V L H - L W - I L C Y
tttcagtgtcaacataaccagtcggtacagctactaagttaacacctgtagaaaatccta
F Q C Q H N Q S V Q L L S - H L - K I L
gctggagaggttaggttagtaccacagcatctctagttgcatgacagccctctacatcaa
A G E V G - Y P Q H L - L H D S P L H Q
agccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacatattagggt
S Q S T H E R D E - L L R G - - T Y - G
aaccattgacttggttaattcattttgaaacccatcatagagatgagtcctacggtaggtca
N H - L G N S F - N P S - R - V Y G R S
tgtcctttgggtatgcctagg
C P L G M P R

FIGURE 123

CCTAGGCATACCCAAAGGACATGACCTACCGTAGACTCATCTCTATGATGGGTTTCAAAATGAATTACCAAGTCAATGGT
.....i.....N..N.....i.....N....
TACCCTAATATGTTTATCACCCGCGAAGAAGCTATTCGTCACGTTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCA
.....i.....N.....N.....
TGCAACTAGAGATGCTGTGGGTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTAACTTAGTAGCTGTACCGA
.....N.....
CTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAGTTAATGCAAAACCTCCACCAGGTGACCAGTTTAAACAT
.....N.....N.....
CTTATACCACTCATGTATAAAGGCTTGCCCTGGAATGTAGTGGTATTAAAGATAGTACAAATGCTCAGTGATACACTGAA
.....N.....N.....N.....
AGGATTGTCAGACAGAGTCGTGTTGCTCCTTTGGGCGCATGGCTTTGAGCTTACATCAATGAAGTACTTTGTCAAGATTG
.....N.....N.....
GACCTGAAAGAACGTGTTGTCTGTGTGACAAACGTGCAACTTGCTTTTCTACTTCATCAGATACTTATGCCTGCTGGAAT
.....N.....
CATTCTGTGGGTTTGGACTATGTCTATAACCCATTTATGATTGATGTTTCAGCAGTGGGGCTTTACGGGTAACCTTCAGAG
.....N.....N.....N.....
TAACCATGACCAACATTGCCAGGTACATGGAAATGCACATGTGGCTAGTTGTGATGCTATCATGACTAGATGTTTAGCAG
.....N.....N.....N.....N.....N.....i.....N.....
TCCATGAGTGCTTTGTTAAGCGCGTTGATTGGTCTGTTGAATACCCTATTATAGGAGATGAACTGAGGGTTAATTCTGCT
...N.....N.....
TGCAGAAAAGTACAACACATGGTTGTGAAGTCTGCATTGCTTGCTGATAAGTTTCCAGTTCTTCATGACATAGGAAATCC
.....i.....N.....
AAAGGCTATCAAGTGTGTGCCCTCAGGCTGAAGTAGAATGGAAGTTCTACGATGCTCAGCCATGTAGTGACAAAGCTTACA
.....N.....N.....N.....
AAATAGAGGAACTCTTCTATTCTTATGCTATACATCACGATAAATTCAGTGATGGTGTTTGTGTTTGGAAATTGTAAC
.....N.....N.....
GTTGATCGTTACCCAGCCAATGCAATTGTGTGTAGGTTTGACACAAGAGTCTTGTCAAACCTGAACTTACCAGGCTGTGA
.....N.....N.....
TGGTGGTAGTTTGTATGTGAATAAGCATGCATTCCACACTCCAGCTTTCGATAAAAGTGCATTTACTAATTTAAAGCAAT
.....N.....N.....
TGCCTTTCTTTTACTATTCTGATAGTCCTTGTGAGTCTCATGGCAAACAAGTAGTGTGCGATATTGATTATGTTCCACTC
.....i.....N.....
AAATCTGCTACGTGTATTACACGATGCAATTTAGGTGGTGTGTTGTCAGACACCATGCAAATGAGTACCGACAGTACTT
.....N.....N.....N.....
GGATGCATATAATATGATGATTTCTGCTGGATTTAGCCTATGGATTTACAAACAATTTGATACTTATAACCTGTGGAATA
..N.....N..N.....N.....
CATTTACCAGGTTACAGAGTTTA **SEQ ID NO: 10084**
.....

FIGURE 123 (contd.)

Pos	Score	Pred
21	0.651	Yes
45	0.354	-
48	0.387	-
60	0.590	Yes
76	0.470	-
90	0.676	Yes
145	0.192	-
160	0.410	-
172	0.290	-
247	0.221	-
286	0.219	-
333	0.373	-
355	0.178	-
381	0.286	-
439	0.405	-
459	0.204	-
547	0.289	-
580	0.447	-
597	0.449	-
604	0.290	-
646	0.427	-
667	0.427	-
673	0.208	-
679	0.317	-
694	0.180	-
702	0.554	Yes
710	0.151	-
724	0.384	-
778	0.151	-
819	0.711	Yes
865	0.306	-
917	0.230	-
931	0.214	-
941	0.190	-
985	0.274	-
1012	0.368	-
1060	0.206	-
1120	0.193	-
1135	0.185	-
1147	0.431	-
1240	0.562	Yes
1270	0.377	-
1304	0.190	-
1336	0.353	-
1342	0.312	-
1363	0.213	-
1374	0.178	-
1377	0.096	-
1400	0.056	-

FIGURE 124

Sequences:		(bits)
Value		
gi 74827 pir VFIHJH genome polyprotein 1b - murine hepatit...	638	0.0
gi 14917044 sp P29982 RRPB_CVMJH RNA-directed RNA polymeras...	637	0.0
gi 26007546 ref NP_068668.2 ORFlab polyprotein [Murine hep...	637	0.0
gi 7769342 gb AAF69332.1 AF208066_2 RNA-directed RNA polyme...	637	0.0
gi 6625761 gb AAF19384.1 AF201929_2 RNA-directed RNA polyme...	637	0.0
gi 2641128 gb AAB86818.1 RNA-directed RNA polymerase [muri...	635	0.0
gi 4377413 emb CAA36202.1 open reading frame 1b (AA 1-2733...	634	0.0
gi 133592 sp P16342 RRPB_CVMA5 RNA-DIRECTED RNA POLYMERASE ...	634	0.0
gi 26008080 ref NP_150073.2 orflab polyprotein [Bovine cor...	633	e-
180		
gi 15077820 gb AAK83365.1 replicase [bovine coronavirus]	633	e-
180		
gi 18033972 gb AAL57305.1 replicase [bovine coronavirus]	633	e-
180		
gi 7769353 gb AAF69342.1 AF208067_2 RNA-directed RNA polyme...	633	e-
180		
gi 17529672 gb AAL40397.1 AF220295_2 RNA polymerase 1b [bov...	623	e-
177		
gi 25121571 ref NP_740618.1 coronavirus nsp11 [Murine hepa...	622	e-
177		
gi 26008092 ref NP_742140.1 coronavirus nsp11 [Bovine coro...	617	e-
175		
gi 10242469 ref NP_066134.1 ORFlab polyprotein; frameshift...	575	e-
163		
gi 14149033 emb CAC39112.1 replicase polyprotein lab [Avia...	575	e-
163		
gi 458735 emb CAA83018.1 potential chimeric protein [Avian...	570	e-
161		
gi 133594 sp P26314 RRPB_IBVB RNA-DIRECTED RNA POLYMERASE (...)	570	e-
161		
gi 29293454 gb AAO67706.1 ORF1b polyprotein [Avian infecti...	565	e-
160		
gi 25121555 ref NP_740631.1 coronavirus nsp11 [Avian infec...	559	e-
158		
gi 9635157 ref NP_058422.1 replicase [Transmissible gastro...	545	e-
153		
gi 19387582 ref NP_598309.1 Pol1 [porcine epidemic diarrhe...	541	e-
152		
gi 12175747 ref NP_073549.1 replicase polyprotein lab [Hum...	535	e-
151		
gi 133591 sp P18458 RRPB_BEV RNA-directed RNA polymerase (O...	50	8e-
05		
gi 1513061 dbj BAA13323.1 cyanoprotein alpha subunit precu...	35	3.7

Alignments

>gi|74827|pir||VFIHJH genome polyprotein 1b - murine hepatitis virus
 (strain JHM)
 Length = 2731

Score = 638 bits (1645), Expect = 0.0
 Identities = 287/481 (59%), Positives = 366/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HATRD++GTN PLQ
 Sbjct: 1585 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAEGAHATRDSIGTNFPLQ
 1644

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + A+ PPG+QFKHL+PLM +G W+VVRI+IVQ
 Sbjct: 1645 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLVPLMSRQKWDVVRIRIVQ
 1704

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
 MLSD L L+D VV V WA FELT ++YF K+G E C +C+KRATCF++ + Y CW
 Sbjct: 1705 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGKEVVCVCKRATCFNSRTGYGCWR
 1764

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
 Sbjct: 1765 HSYSCDYLYNPLIVDIQQWGYTGSLSNHDPICSVHKGAHVASSDAIMTRCLAVHDCFK
 1824

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
 Sbjct: 1825 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF
 1882

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVLS
 Sbjct: 1883 KFYDASPV---VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLSK
 1939

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425
 LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL
 Sbjct: 1940 LNLPGCNGGSLYVNKHAFHTNPFTRA AFENLKPMFPFFYYSDTPCVYMEGMESKQVDYVPL
 1999

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS
 Sbjct: 2000 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS
 2059

Query: 486 L 486
 L
 Sbjct: 2060 L 2060

>gi|14917044|sp|P29982|RRPB_CVMJH RNA-directed RNA polymerase (ORF1B)
 gi|7583321|gb|AAA46458.2| open reading frame 1b [murine hepatitis virus]
 Length = 2731

Score = 637 bits (1644), Expect = 0.0
 Identities = 287/481 (59%), Positives = 366/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HATRD++GTN PLQ
 Sbjct: 1585 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAEGAHAATRDSIGTNFPLQ
 1644

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + A+ PPG+QFKHL+PLM +G W+VVRI+IVQ
 Sbjct: 1645 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLVPLMSRGQKWDVVRIRIVQ
 1704

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
 MLSD L L+D VV V WA FELT ++YF K+G E C +C+KRATCF++ + Y CW
 Sbjct: 1705 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGKEVVCVCNKRATCFNSRTGGYGCWR
 1764

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
 Sbjct: 1765 HSYSCDYLYNPLIVDIQQWGYTGSLSNHDPICSVHKGAVASSDAIMTRCLAVHDCFCK
 1824

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
 Sbjct: 1825 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF
 1882

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVLS
 Sbjct: 1883 KFYDASPV---VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLSK
 1939

Query: 366 LNLPGCDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDYVPL 425
 LNLPGC+GGSLYVNKHAFT F ++AF NLK +PFFYYSD+PC +DYVPL
 Sbjct: 1940 LNLPGCNGGSLYVNKHAFTNPFTRAAFENLKPMPPFFYYSDTPCVMEGMESKQVDYVPL
 1999

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDYTNLWNTFTRLQS 485
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS
 Sbjct: 2000 RSATCITRCNLGGAVCLKHAEEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS
 2059

Query: 486 L 486
 L
 Sbjct: 2060 L 2060

>gi|26007546|ref|NP_068668.2| ORFlab polyprotein [Murine hepatitis virus]
 Length = 7178

Score = 637 bits (1644), Expect = 0.0
 Identities = 286/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ
 Sbjct: 6032 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAEGAHAIRDSIGTNFPLQ
 6091

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ
 Sbjct: 6092 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLIPLMSRGQKWDVVRIIRIVQ
 6151

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
 MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW
 Sbjct: 6152 MLSDHLADLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGGYGCWR
 6211

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
 Sbjct: 6212 HSYSCDYLYNPLIVDIQQWGYTGSLTSNHDPICSVHKGAVASSDAIMTRCLAVHDCFK
 6271

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKSALLADKFPVLHDIGNPKAIKCVPAEVEW 305
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
 Sbjct: 6272 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF
 6329

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLN 365
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+
 Sbjct: 6330 KFYDASPV---VKSVMQFVYKYEAHKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK
 6386

Query: 366 LNLPGCDGGSLYVKNHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425
 LNLPGC+GGSLYVKNHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL
 Sbjct: 6387 LNLPGCNGGSLYVKNHAFHTSPFTRA AFENLKPMPPFFYYSDTPCVMEGMESKQVDYVPL
 6446

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS
 Sbjct: 6447 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS
 6506

Query: 486 L 486
 L
 Sbjct: 6507 L 6507

>gi|7769342|gb|AAF69332.1|AF208066_2 RNA-directed RNA polymerase [murine
 hepatitis virus]
 Length = 2732

Score = 637 bits (1644), Expect = 0.0
 Identities = 287/481 (59%), Positives = 366/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FITR+EAIR VRAW+GFD EG HATRD++GTN PLQ
 Sbjct: 1586 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIRRVRAWVGFDAEGAHATRDSIGTNFPLQ
 1645

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + A+ PPG+QFKHL+PLM +G W+VVRI+IVQ

Sbjct: 1646 LGFSTGIDFVVEATGMFAERDGYVFKKAVARAPPGEQFKHLVPLMSRGQKWDVVRIIRIVQ
1705

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
MLSD L L+D VV V WA FELT ++YF K+G E C +C+KRATCF++ + Y CW

Sbjct: 1706 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGKEVVCVNCNKRATCFNSRTGYGCWR
1765

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K

Sbjct: 1766 HSYSCDYLYNPLIVDIQQWGYTGSLSNHDLICSVHKGAVASSDAIMTRCLAVHDCFCCK
1825

Query: 246 RVDWSVEYPIIGDELRVNSACRQVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305
V+WS+EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++

Sbjct: 1826 SVNWSLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF
1883

Query: 306 KFYDAQPCSDKAYKIEELFYSYAIHHDKFTDGVCLFWNCNVDYRYPANAIVCRFDTRVLSN 365
KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+

Sbjct: 1884 KFYDASPV---VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDKYPANAVCRFDTRVLNK
1940

Query: 366 LNLPGCDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVSDIDYVPL 425
LNLPGC+GGSLYVNKHAFT F ++AF NLK +PFFYYSD+PC +DYVPL

Sbjct: 1941 LNLPGCNGGSLYVNKHAFTSPFTRA AFENLKPMFPFFYYSDTPCVYMEGMESKQVDYVPL
2000

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDYTNLWNTFTRLQS 485
+SATCITRCNLGGAVC HA +YR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS

Sbjct: 2001 RSATCITRCNLGGAVCLKHAEDYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS
2060

Query: 486 L 486
L

Sbjct: 2061 L 2061

>gi|6625761|gb|AAF19384.1|AF201929_2 RNA-directed RNA polymerase [murine
hepatitis virus strain 2]

gi|7739595|gb|AAF68920.1|AF207902_2 RNA-directed RNA polymerase [murine
hepatitis virus strain ML-11]

Length = 2733

Score = 637 bits (1643), Expect = 0.0

Identities = 287/481 (59%), Positives = 366/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDVGTNLPLQ 65
+TY RLIS+MGFK++ ++GY +FTR+EAIR VRAW+GFD EG HATRD++GTN PLQ

Sbjct: 1587 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIRRVRAWVGFD AEGAHATRDSIGTNFPLQ
1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
LGFSTG++ V TG + F + A+ PPG+QFKHL+PLM +G W+VVRI+IVQ

Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKKAVARAPPGEQFKHLVPLMSRGQKWDVVRIIRIVQ
1706

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
MLSD L L+D VV V WA FELT ++YF K+G E C +C+KRATCF++ + Y CW

Sbjct: 1707 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGKEVVCVKNRATCFNSRTGGYGCWR
1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K

Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLSNHDLCVHKGAVHASSDAIMTRCLAVHDCFCCK
1826

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305
V+WS+EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++

Sbjct: 1827 SVNWSLEYPIISNEVSVNTSCRLLQRMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF
1884

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+

Sbjct: 1885 KFYDASPV---VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDKYPANAVCRFDTRVLNK
1941

Query: 366 LNLPGCDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425
LNLPGC+GGSLYVNKHAFT F ++AF NLK +PFFYYSD+PC +DYVPL

Sbjct: 1942 LNLPGCNGGSLYVNKHAFTSPFTRAFAENLKPMPPFFYYSDTPCVYMEGMESKQVDYVPL
2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDYTNLWNTFTRLQS 485
+SATCITRCNLGGAVC HA +YR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS

Sbjct: 2002 RSATCITRCNLGGAVCLKHAEDYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS
2061

Query: 486 L 486
L

Sbjct: 2062 L 2062

>gi|2641128|gb|AAB86818.1| RNA-directed RNA polymerase [murine hepatitis
virus]

Length = 2733

Score = 635 bits (1637), Expect = 0.0

Identities = 286/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDAVGTNLPLQ 65
+TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ

Sbjct: 1587 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAEGAHAIRDSIGTNFPLQ
1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ

Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLIPLMSRGQKWDVVRIIRIVQ
1706

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
 MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW
 Sbjct: 1707 MLSDHLADLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGGYGCWR
 1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
 Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLSNHDPICSVHKGAVASSDAIMTRCLAVHDCFCK
 1826

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKSALLADKFPVLHDIGNPKAIKCVPAEVEW 305
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
 Sbjct: 1827 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF
 1884

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+
 Sbjct: 1885 KFYDASPV---VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK
 1941

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVSDIDYVPL 425
 LNLPGC+GGSLYVNKHAFHT F ++AF NLK +PFFYYSD+PC +DYVPL
 Sbjct: 1942 LNLPGCNGGSLYVNKHAFHTSPFTRA AFENLKPMFPFFYYSDTPCVMEGMESKQVDYVPL
 2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS
 Sbjct: 2002 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS
 2061

Query: 486 L 486
 L
 Sbjct: 2062 L 2062

>gi|4377413|emb|CAA36202.1| open reading frame 1b (AA 1-2733) [Murine
 hepatitis virus]
 Length = 2733

Score = 634 bits (1636), Expect = 0.0
 Identities = 286/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDAVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FTR+EAI+ VRAW+GFD EG HA RD++GTN PLQ
 Sbjct: 1587 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFD AEGAHAIRDSIGTNFPLQ
 1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ
 Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLIPLMSRQKWDVVRIRIVQ
 1706

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
 MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW

Sbjct: 1707 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGYGWCWR
1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K

Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLTSNHDPICSVHKGAVASSDAIMTRCLAVHDCFCCK
1826

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305
V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++

Sbjct: 1827 SVNWNLEYPIISNEVSVNTSRLQLQRMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF
1884

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+

Sbjct: 1885 KFYDASPV--VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDPYANAVVCRFDTRVLNK
1941

Query: 366 LNLPGCDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDDIDYVPL 425
LNLPGC+GGSLYVNKHAFT F ++AF NLK +PFFYYSD+PC +DYVPL

Sbjct: 1942 LNLPGCNGGSLYVNKHAFTSPFTRAAFENLKPMFPFFYYSDTPCVMEGMESKQVDYVPL
2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
+SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS

Sbjct: 2002 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS
2061

Query: 486 L 486
L

Sbjct: 2062 L 2062

>gi|133592|sp|P16342|RRPB_CVMA5 RNA-DIRECTED RNA POLYMERASE (ORF1B)
gi|93916|pir||S15760 genome polyprotein - murine hepatitis virus (strain
A59)

Length = 2733

Score = 634 bits (1636), Expect = 0.0

Identities = 286/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPLQ 65
+TY RLIS+MGFK++ ++GY +FTR+EAI+ VRAW+GFD EG HA RD++GTN PLQ

Sbjct: 1587 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAGAHAIKDSIGTNFPLQ
1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ

Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKAAARAPPGEQFKHLIPLMSRQKWDVVRIRIVQ
1706

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACWN 185
MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW

Sbjct: 1707 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGYGWCWR
1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
 Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGSLTSNHDPICSVHKGAVASSDAIMTRCLAVHDCFCK
 1826

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEW 305
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
 Sbjct: 1827 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF
 1884

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+
 Sbjct: 1885 KFYDASPV---VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDPYANAVVCRFDTRVLNK
 1941

Query: 366 LNLPGCDGGSLYVKNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVSDIDYVPL 425
 LNLPGC+GGSLYVKNKHAFT F ++AF NLK +PFFYYSD+PC +DYVPL
 Sbjct: 1942 LNLPGCNGGSLYVKNKHAFTSPFTRA AFENLKPMFPFFYYSDTPCVMEGMESKQVDYVPL
 2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS
 Sbjct: 2002 RSATCITRCNLGGAVCLKHAEEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS
 2061

Query: 486 L 486
 L
 Sbjct: 2062 L 2062

>gi|26008080|ref|NP_150073.2| orflab polyprotein [Bovine coronavirus]
 Length = 7094

Score = 633 bits (1633), Expect = e-180
 Identities = 284/481 (59%), Positives = 367/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ
 Sbjct: 5948 VTYSRLISLMGFKLDVTLDDGYCKLFITKEEAVKRVRWVGFDAEGAHATRDSIGTNFPLQ
 6007

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ
 Sbjct: 6008 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ
 6067

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
 M +D L LSD VV V WA FELT ++YF K+G E +C +C KRAT +++ + Y CW
 Sbjct: 6068 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVCTKRATAYNSRTGYGWCWR
 6127

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF

Sbjct: 6128 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTRCLAVYDCFCN
6187

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKALLADKFPVLHDIGNPKAIKCVPAEVEW 305
++W+VEYPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++

Sbjct: 6188 NINWNVEYPIISNELSINTSCRVLQRVMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF
6245

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
KFYDAQP ++ L YS+ H D F DG+C+FWNCNVD+YP NA+VCRFDTRVL+N

Sbjct: 6246 KFYDAQPI---VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVDPKPPNAVVCRFDTVLNN
6302

Query: 366 LNLPGCDGGS LYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVSDIDYVPL 425
LNLPGC+GGS LYVNKHAFHT F ++AF +LK +PFFYYSD+PC +DYVPL

Sbjct: 6303 LNLPGCNGGS LYVNKHAFHTKPFSSRAAFEHLKPMPPFFYYSDTPCVYMDGMDAKQVDYVPL
6362

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQS

Sbjct: 6363 KSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTKLQS
6422

Query: 486 L 486
L

Sbjct: 6423 L 6423

>gi|15077820|gb|AAK83365.1| replicase [bovine coronavirus]
Length = 7094

Score = 633 bits (1633), Expect = e-180
Identities = 284/481 (59%), Positives = 367/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDVGTNLPLQ 65
+TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ

Sbjct: 5948 VTYSRLISLMGFKLDVTLDDGYCKLFITKEEAVKRVRWVGFDAGAHATRDSIGTNFPLQ
6007

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ

Sbjct: 6008 LGFSTGIDFVVEATGLFADR DGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ
6067

Query: 126 MLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
M +D L LSD VV V WA FELT ++YF K+G E +C +C KRAT +++ + Y CW

Sbjct: 6068 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVCTKRATAYNSRTGYGCWR
6127

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF

Sbjct: 6128 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTRCLAVYDCFCN
6187

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVKALLADKFPVLHDIGNPKAIKCVPAEVEW 305

++W+VEYPPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++
 Sbjct: 6188 NINWNVEYPPIISNELSINTSCRVLQVRMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF
 6245

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDAQP ++ L YS+ H D F DG+C+FWNCNVD+YP NA+VCRFDTRVL+N

Sbjct: 6246 KFYDAQPI---VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVDKYPPNAVCRFDTRVLNN
 6302

Query: 366 LNLPGCDGGS LYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVS DIDIYVPL 425
 LNLPGC+GGS LYVNKHAFT F ++AF +LK +PFFYYSD+PC +DYVPL

Sbjct: 6303 LNLPGCNGGS LYVNKHAFTKPF SRAAFEHLKPM PFFYYSDTPCVYMDGMDAQVDYVPL
 6362

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
 KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQS

Sbjct: 6363 KSATCITRCNLGGAVCLKHAEEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTKLQS
 6422

Query: 486 L 486

L

Sbjct: 6423 L 6423

>gi|18033972|gb|AAL57305.1| replicase [bovine coronavirus]
 Length = 7094

Score = 633 bits (1633), Expect = e-180

Identities = 284/481 (59%), Positives = 367/481 (76%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISM MGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ

Sbjct: 5948 VTYSRLISLMGFKLDVTL DGYCKLFITKEEAVKRVRWVGFD AEGAHATRDSIGTNFPLQ
 6007

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ

Sbjct: 6008 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ
 6067

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
 M +D L LSD VV V WA FELT ++YF K+G E +C +C KRAT +++ + Y CW

Sbjct: 6068 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVCTKRATAYNSRTGYYGCWR
 6127

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF

Sbjct: 6128 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTRCLAVDCFCN
 6187

Query: 246 RVDWSVEYPPIIGDEL RVNSACRKVQHMVVK SALLADKFPVLHDIGNPKAIKVPQAEVEW 305
 ++W+VEYPPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++

Sbjct: 6188 NINWNVEYPPIISNELSINTSCRVLQVRMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF
 6245

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDAQP ++ L YS+ H D F DG+C+FWNCNVD+YP NA+VCRFDTRVL+N
 Sbjct: 6246 KFYDAQPI---VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVDPKPPNAVVCRFDTRVLNN
 6302

Query: 366 LNLPGCDGGS LYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDIDYVPL 425
 LNLPGC+GGS LYVNKHAFT F ++AF +LK +PFFYYSD+PC +DYVPL
 Sbjct: 6303 LNLPGCNGGS LYVNKHAFTKPF SRAAFEHLKPM PFFYYSDTPCVYMDGMDAKQVDYVPL
 6362

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
 KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQS
 Sbjct: 6363 KSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTKLQS
 6422

Query: 486 L 486
 L
 Sbjct: 6423 L 6423

>gi|7769353|gb|AAF69342.1|AF208067_2 RNA-directed RNA polymerase [murine
 hepatitis virus]
 Length = 2733

Score = 633 bits (1633), Expect = e-180
 Identities = 285/481 (59%), Positives = 364/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMGMFYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDVGTNLPLQ 65
 ++Y RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ
 Sbjct: 1587 VSYRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFD AEGAHAIRDSIGTNFPLQ
 1646

Query: 66 LGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ
 Sbjct: 1647 LGFSTGIDFVVEATGMFAERDGYVFKKAAARAPPGEQFKHLIPLMSRGQKWDVVRIRIVQ
 1706

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
 MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW
 Sbjct: 1707 MLSDHLVDLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGYG CWR
 1766

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
 Sbjct: 1767 HSYSCDYLYNPLIVDIQQWGYTGS LTSNHD PICSVHKGAHVASSDAIMTRCLAVHDCFCK
 1826

Query: 246 RVDWSVEYPIIGDEL RVNSACRKVQH MVVKSALLADKFPVLHDIGNPKAIKCV PQAEVEW 305
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
 Sbjct: 1827 SVNWNLEYPIISNEVSVNTS RLLQ RVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF
 1884

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVD+YPANA+VCRFDTRVL+

Sbjct: 1885 KFYDASPV---VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDKYPANAVVCRFDTRVLNK
1941

Query: 366 LNLPGCDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425
LNLPGC+GGSLYVNKHAFT F ++AF NLK +PFFYYSD+PC +DYVPL

Sbjct: 1942 LNLPGCNGGSLYVNKHAFTSPFTRA AFENLKPMPPFFYYSDTPCVMEGMESKQVDYVPL
2001

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
+SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQS

Sbjct: 2002 RSATCITRCNLGGAVCLKHAEEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQS
2061

Query: 486 L 486
L

Sbjct: 2062 L 2062

>gi|17529672|gb|AAL40397.1|AF220295_2 RNA polymerase 1b [bovine
coronavirus]

Length = 2685

Score = 623 bits (1607), Expect = e-177

Identities = 282/481 (58%), Positives = 365/481 (75%), Gaps = 5/481 (1%)

Query: 6 MTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
+TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ

Sbjct: 1574 VTYSRLISLMGFKLDVTLDDGYCKLFITKEEAVKRVRAWVGFDAEGA HATRDSIGTNFPLQ
1633

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ

Sbjct: 1634 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ
1693

Query: 126 MLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
M +D L LSD VV V WA FELT ++YF K+G E +C + KRAT +++ + Y CW

Sbjct: 1694 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVSTKRATAYNSRTGYGWCWR
1753

Query: 186 HSVGFDYVYNPFMIDVQWGF TGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
HSV DY+YNP ++D+QWGG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF

Sbjct: 1754 HSVTCDYLYNPLIVDIQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTRCLAVYDCFCN
1813

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHVMVKSALLADKFPVLHDIGNPKAIKCVPAEVEW 305
++W+VEYPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++

Sbjct: 1814 NINWNVEYPIISNELSINTSCRVLQRVMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF
1871

Query: 306 KFYDAQPCSDKAYKIEELFYSYAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSN 365
KFYDAQP ++ L Y + H D F DG+C+FWNCNV D+YP NA+VCRFDTRVL+N

Sbjct: 1872 KFYDAQPI---VKSVMKLLYFFEAHKDSFKDGLCMFWNCNVDKYPPNAVVCRFDTRVLNN
1928

Query: 366 LNLPGCDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425
 LNLPGC+GGSLYVNKHAFT F ++AF +LK +PFFYYSD+PC +DYVPL
 Sbjct: 1929 LNLPGCNGGSLYVNKHAFTKPFSSRAAFEHLKPMPPFFYYSDTPCVYMDGMDAKQVDYVPL
 1988

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQS 485
 KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQS
 Sbjct: 1989 KSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTKLQS
 2048

Query: 486 L 486
 L
 Sbjct: 2049 L 2049

>gi|25121571|ref|NP_740618.1| coronavirus nsp11 [Murine hepatitis virus]
 Length = 521

Score = 622 bits (1603), Expect = e-177
 Identities = 284/479 (59%), Positives = 362/479 (75%), Gaps = 5/479 (1%)

Query: 6 MTYRRLLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FITR+EAI+ VRAW+GFD EG HA RD++GTN PLQ
 Sbjct: 48 VTYSRLISLMGFKLDLTLDGYCKLFITRDEAIKRVRAWVGFDAGAHAIKDSIGTNFPLQ 107

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + A+ PPG+QFKHLIPLM +G W+VVRI+IVQ
 Sbjct: 108 LGFSTGIDFVVEATGMFAERDGYVFKAAARAPPGEQFKHLIPLMSRGQKWDVVRIRIVQ 167

Query: 126 MLSDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDYACWN 185
 MLSD L L+D VV V WA FELT ++YF K+G E C +C KRATCF++ + Y CW
 Sbjct: 168 MLSDHLADLADSVVLVTWAASFELTCLRYFAKVGREVVCSVCTKRATCFNSRTGYGVCWR 227

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HS DY+YNP ++D+QQWG+TG+L SNHD C VH AHVAS DAIMTRCLAVH+CF K
 Sbjct: 228 HSYSCDYLYNPLIVDIQQWGYTGSLSNHDPICSVHKGAHVASSDAIMTRCLAVHDCFCCK 287

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVEW 305
 V+W++EYPII +E+ VN++CR +Q ++ ++A+L +++ V +DIGNPK + CV ++
 Sbjct: 288 SVNWNLEYPIISNEVSVNTSCRLLRVMFRAAMLCNRYDVCYDIGNPKGLACVKG--YDF 345

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLN 365
 KFYDA P +++ Y Y H D+F DG+C+FWNCNVDRYPANA+VCRFDTRVL+
 Sbjct: 346 KFYDASPV---VKSVMQFVYKYEAKDQFLDGLCMFWNCNVDPANAVVCRFDTRVLNK 402

Query: 366 LNLPGCDGGSLYVNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425
 LNLPGC+GGSLYVNKHAFT F ++AF NLK +PFFYYSD+PC +DYVPL
 Sbjct: 403 LNLPGCNGGSLYVNKHAFTSPFTRAFFENLKPMPPFFYYSDTPCVYMEGMESKQVDYVPL 462

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
 +SATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFTRLQ
 Sbjct: 463 RSATCITRCNLGGAVCLKHAEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTRLQ 521

>gi|26008092|ref|NP_742140.1| coronavirus nsp11 [Bovine coronavirus]

Length = 521

Score = 617 bits (1590), Expect = e-175

Identities = 282/479 (58%), Positives = 365/479 (76%), Gaps = 5/479 (1%)

Query: 6 MTYRRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRRAWIGFDVEGCHATRDAVGTNLPLQ 65
 +TY RLIS+MGFK++ ++GY +FIT+EEA++ VRAW+GFD EG HATRD++GTN PLQ
 Sbjct: 48 VTYSRLISLMGFKLDVTLDDGYCKLFITKEEAVKRVRAWVGFDAGAHATRDSIGTNFPLQ 107

Query: 66 LGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 125
 LGFSTG++ V TG + F + AK PPG+QFKHLIPLM +G W+VVR +IVQ
 Sbjct: 108 LGFSTGIDFVVEATGLFADRDGYSFKKAVAKAPPGEQFKHLIPLMTRGQRWDVVRPRIVQ 167

Query: 126 MLSDTLKGLSDRVVFWLWAGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWN 185
 M +D L LSD VV V WA FELT ++YF K+G E +C +C KRAT +++ + Y CW
 Sbjct: 168 MFADHLIDLSDCVVLVTWAANFELTCLRYFAKVGREISCNVCTKRATAYNSRTGYGWCWR 227

Query: 186 HSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVK 245
 HSV DY+YNP ++D+QQWG+ G+L SNHD +C VH AHVAS DAIMTRCLAV++CF
 Sbjct: 228 HSVTCDYLYNPLIVDIQQWGYIGSLSSNHDLYCSVHKGAHVASSDAIMTRCLAVYDCFCN 287

Query: 246 RVDWSVEYPIIGDELRVNSACRKVQHMVVSALLADKFPVLHDIGNPKAIKCVPAEVEW 305
 ++W+VEYPII +EL +N++CR +Q +++K+A+L +++ + +DIGNPKAI CV + ++
 Sbjct: 288 NINWNVEYPIISNELSINTSCRVLQRVMLKAAMLCNRYTLCYDIGNPKAIACV--KDFDF 345

Query: 306 KFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLEFWNCNVDRIYANAIVCRFDTRVLSN 365
 KFYDAQP ++ L YS+ H D F DG+C+FWNCNVD+YP NA+VCRFDTRVL+N
 Sbjct: 346 KFYDAQPI---VKS VKTLLYSFEAHKDSFKDGLCMFWNCNVDKYPNAVCRFDTRVLNN 402

Query: 366 LNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPL 425
 LNLPGC+GGSLYVNKHAFHT F ++AF +LK +PFFYYSD+PC +DYVPL
 Sbjct: 403 LNLPGCNGGSLYVNKHAFHTKPFSSRAAFEHLKMPFFYYSDTPCVYMDGMDAKQVDYVPL 462

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
 KSATCITRCNLGGAVC HA EYR+YL++YN +AGF+ W+YK FD YNLWNTFT+LQ
 Sbjct: 463 KSATCITRCNLGGAVCLKHAEEYREYLESYNTATTAGFTFWVYKTFDFYNLWNTFTKLQ 521

>gi|10242469|ref|NP_066134.1| ORFlab polyprotein; frameshift product
 [Avian infectious bronchitis
 virus]
 Length = 6629

Score = 575 bits (1482), Expect = e-163

Identities = 262/482 (54%), Positives = 344/482 (71%), Gaps = 5/482 (1%)

Query: 5 DMTYRRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRRAWIGFDVEGCHATRDAVGTNLPL 64
 ++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP
 Sbjct: 5515 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIGTNLPF
 5574

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIVQ 124
 Q+GFSTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV
 Sbjct: 5575 QVGSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAPKWHVIRPRIV
 5634

Query: 125 QMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACW 184
 QML+D L +SD VVFFV W HG ELT+++YFVKIG E+ C C RAT F++ + YACW
 Sbjct: 5635 QMLADNLCNVSDCVVFTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSTQAYACW
 5693

Query: 185 NHSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
 H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VHG+AHVAS DAIMTRCLA++ F
 Sbjct: 5694 KHCLGFDFVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAVASVDAIMTRCLAINNAFC
 5753

Query: 245 KRVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVE 304
 + V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V
 Sbjct: 5754 QDVNWDLTYPHIANEDEVNSSCRYLQRMVNLACVDALKVNVVYDIGNPKGIKCVRRGDVN
 5813

Query: 305 WKFYDAQPCSDKAYKIEELFYSYAIHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364
 ++FYD P + E Y Y H DKF DG+C+FWNCNVDP YP N++VCR+DTR LS
 Sbjct: 5814 FRFYDKNPIVRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNLVCRYDTRNLS
 5870

Query: 365 NLNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVP 424
 NLPGC+GGSLYVNKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V
 Sbjct: 5871 VFNLPGCNGGSLYVNKHAFYTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS
 5929

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
 L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ
 Sbjct: 5930 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ
 5989

Query: 485 SL 486
 S+
 Sbjct: 5990 SI 5991

>gi|14149033|emb|CAC39112.1| replicase polyprotein lab [Avian infectious
 bronchitis virus (strain
 Beaudette CK)]
 Length = 6629

Score = 575 bits (1482), Expect = e-163
 Identities = 262/482 (54%), Positives = 344/482 (71%), Gaps = 5/482 (1%)

Query: 5 DMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPL 64
 ++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP
 Sbjct: 5515 EITYKHLISLLGFKMSVÑVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIGTNLPF
 5574

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIV 124
 Q+GFASTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV
 Sbjct: 5575 QVGFASTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAKPWHVIRPRIV
 5634

Query: 125 QMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDITYACW 184

QML+D L +SD VV FV W HG ELT+++YFVKIG E+ C C RAT F++ + YACW
 Sbjct: 5635 QMLADNLCNVSDCVVFTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW
 5693

Query: 185 NHSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
 H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VH G+AHVAS DAIMTRCLA++ F
 Sbjct: 5694 KHCLGFDVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAHVASVDAIMTRCLAINNAFC
 5753

Query: 245 KRVDWSVEYPIIGDELRVNSACRQVQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVE 304
 + V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V
 Sbjct: 5754 QDVNWDLTYPHIANEDEVNSSCRYLQRMVNLACVDALKVNVVVDIGNPKGIKCVRRGDVN
 5813

Query: 305 WKFYDAQPCSDKAYKIEELFYSYAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364
 ++FYD P + E Y Y H DKF DG+C+FWNCNVD YP N++VCR+DTR LS
 Sbjct: 5814 FRFYDKNPIVRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNSLVCRYDTRNLS
 5870

Query: 365 NLNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSDIDYVP 424
 NLPGC+GGSLYVNKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V
 Sbjct: 5871 VFNLPGCNGGSLYVNKHAFYTPKFDRISFRNLKAMPFFFFYDSSPCETIQVDGVAQ-DLVS
 5929

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
 L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ
 Sbjct: 5930 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ
 5989

Query: 485 SL 486
 S+
 Sbjct: 5990 SI 5991

>gi|458735|emb|CAA83018.1| potential chimeric protein [Avian infectious
 bronchitis virus]
 Length = 2155

Score = 570 bits (1470), Expect = e-161
 Identities = 262/482 (54%), Positives = 344/482 (71%), Gaps = 5/482 (1%)

Query: 5 DMTYRRLISMGMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDAVGTNLPL 64
 ++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLPL
 Sbjct: 1596 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIGTNLPL
 1655

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIV 124
 Q+GFSTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV
 Sbjct: 1656 QVGFSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAKPWHVIRPRIV
 1715

Query: 125 QMLSDTLKGLSDRVVFWLWAGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACW 184
 QML+D L +SD VV FV W HG ELT+++YFVKIG E+ C C RAT F++ + YACW
 Sbjct: 1716 QMLADNLCNVSDCVVFTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW
 1774

Query: 185 NHSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
 H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VHG+AHVAS DAIMTRCLA++ F
 Sbjct: 1775 KHCLGFDFVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAVASVDAIMTRCLAINNAFC
 1834

Query: 245 KRVDWSVEYPIIGDELRVNSACRKYQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVE 304
 + V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V
 Sbjct: 1835 QDVNWDLTYPHIANEDEVNSSCRYLQRMVNLACVDALKVNVVYDIGNPKGIKCVRRGDVN
 1894

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLEFWNCNVDRYPANAIVCRFDTRVLS 364
 ++FYD P + E Y Y H DKF DG+C+FWNCNVD YP N++VCR+DTR LS
 Sbjct: 1895 FRFYDKNPIVRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNSLVCRYDTRNLS
 1951

Query: 365 NLNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVP 424
 NLPGC+GGSLYVNKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V
 Sbjct: 1952 VFNLPGCNGGSLYVNKHAFYTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS
 2010

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
 L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ
 Sbjct: 2011 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ
 2070

Query: 485 SL 486
 S+
 Sbjct: 2071 SI 2072

>gi|133594|sp|P26314|RRPB_IBVB RNA-DIRECTED RNA POLYMERASE (ORF1B)
 gi|74826|pir||VFIHB2 genome polyprotein - avian infectious bronchitis
 virus (strain
 Beaudette)
 gi|292953|gb|AAA70234.1| pol protein [Avian infectious bronchitis virus]
 gi|331173|gb|AAA46224.1| ORF1b [Avian infectious bronchitis virus]
 Length = 2652

Score = 570 bits (1469), Expect = e-161
 Identities = 262/482 (54%), Positives = 344/482 (71%), Gaps = 5/482 (1%)

Query: 5 DMTYRRRLISMGEKMNQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDAVGTNLPL 64
 ++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP
 Sbjct: 1538 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWGFDVEATHACGTNIGTNLPF
 1597

Query: 65 QLGSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIV 124
 Q+GFSTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV
 Sbjct: 1598 QVGFSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGQFNHLRVLFKSAKPWHVIRPRIV
 1657

Query: 125 QMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACW 184
 QML+D L +SD VVFEV W HG ELT+++YFVKIG E+ C C RAT F++ + YACW

Sbjct: 1658 QMLADNLCNVSDCVVFWTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW
1716

Query: 185 NHSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VHG+AHVAS DAIMTRCLA++ F

Sbjct: 1717 KHCLGFDVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAVASVDAIMTRCLAINNAFC
1776

Query: 245 KRVDWSVEYPIIGDELRVNSACRKYQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVE 304
+ V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V

Sbjct: 1777 QDVNWDLTYPHIANEDEVNSSCRYLQRMVNLACVDALKVNVVVDIGNPKGIKCVRRGDVN
1836

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364
++FYD P + E Y Y H DKF DG+C+FWNCNVD YP N++VCR+DTR LS

Sbjct: 1837 FRFYDKNPIVRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNSLVCRYDTRNLS
1893

Query: 365 NLNLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHKGQVVSDDIDYVP 424
NLPGC+GGSLYVNKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V

Sbjct: 1894 VFNLPGCNGGSLYVNKHAFYTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS
1952

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ

Sbjct: 1953 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ
2012

Query: 485 SL 486
S+

Sbjct: 2013 SI 2014

>gi|29293454|gb|AA067706.1| ORF1b polyprotein [Avian infectious bronchitis
virus]

Length = 2649

Score = 565 bits (1455), Expect = e-160

Identities = 261/482 (54%), Positives = 342/482 (70%), Gaps = 8/482 (1%)

Query: 5 DMTYRRLISMGMFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDAVGTNLPL 64
++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP

Sbjct: 1538 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWVGFDVEATHACGTNIGTNLPP
1597

Query: 65 QLGSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIV 124
Q+GFSTG + V P G +DT F VN+K PPG+QF HL L PW+V+R +IV

Sbjct: 1598 QVGFSTGADFVVTPEGLIDTSIGNNFEPVNSKAPPGEQFNHLRALFKSAKPWHVIRPRIV
1657

Query: 125 QMLSDTLKGLSDRVVFWLWAGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACW 184
QML+D L +SD VVFW W HG ELT+++YFVKIG E+ C C RAT F++ + YACW

Sbjct: 1658 QMLADNLCNVSDCVVFWTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW
1716

Query: 185 NHSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
 H +G VYNP ++D+QQWG++GNLQ NHD HC VH+AHVAS DA+MTRCLA++ F
 Sbjct: 1717 RHCLG---VYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAAHVASADAVMTRCLAINNAFC
 1773

Query: 245 KRVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVE 304
 K V+W ++YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V
 Sbjct: 1774 KDVNWELQYPHIANEDEVNSSCRYLQRMVYNACVDALKVNVVYDIGNPKGIKCVRRGDVN
 1833

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364
 ++FYD P + E Y Y+ H DKF DG+C+FWNCNVDP YP N++VCR+DTR LS
 Sbjct: 1834 FRFYDKNPIVPNVKQFE---YDYSQHKDKFADGLCMFWNCNVDCYPENSLVCRYDTRNLS
 1890

Query: 365 NLNLPGLGGSGLYVKNKHAFTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVSDIDYVP 424
 NLPGC+GGSGLYVKNKHAFTP FD+ +F NLK +PFF+Y SPCE+ V+ D V
 Sbjct: 1891 VFNLPGLGGSGLYVKNKHAFTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS
 1949

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
 L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ F+ YNLW F+ LQ
 Sbjct: 1950 LATKDCITKCNIGGAVCKKHAQMYAEFVSYNAAVTAGFTFWVTNNFNPYNLWKNFSAQ
 2009

Query: 485 SL 486
 S+
 Sbjct: 2010 SI 2011

>gi|25121555|ref|NP_740631.1| coronavirus nspl1 [Avian infectious
 bronchitis virus]
 Length = 521

Score = 559 bits (1440), Expect = e-158
 Identities = 261/480 (54%), Positives = 342/480 (71%), Gaps = 5/480 (1%)

Query: 5 DMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDVGTNLPL 64
 ++TY+ LIS++GFKM+ V G NMFITR+EAIR+VR W+GFDVE HA +GTNLP
 Sbjct: 47 EITYKHLISLLGFKMSVNVEGCHNMFITRDEAIRNVRGWGFDVEATHACGTNIGTNLPF 106

Query: 65 QLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIV 124
 Q+GFSTG + V P G VDT F VN+K PPG+QF HL L PW+V+R +IV
 Sbjct: 107 QVGFSTGADFVVTPEGLVDTSIGNNFEPVNSKAPPGEQFNHLRVLFKSAKPWHVIRPRIV 166

Query: 125 QMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACW 184
 QML+D L +SD VVFV W HG ELT+++YFVKIG E+ C C RAT F++ + YACW
 Sbjct: 167 QMLADNLCNVSDCVVFTWCHGLELTTLRYFVKIGKEQVCS-CGSRATTFNSHTQAYACW 225

Query: 185 NHSVGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFV 244
 H +GFD+VYNP ++D+QQWG++GNLQ NHD HC VH+AHVAS DAIMTRCLA++ F
 Sbjct: 226 KHCLGFDFVYNPLLVDIQQWGYSGNLQFNHDLHCNVHGHAAHVASVDAIMTRCLAINNAFC 285

Query: 245 KRVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPAEVE 304
 + V+W + YP I +E VNS+CR +Q M + + + A K V++DIGNPK IKCV + +V

Sbjct: 286 QDVNWDLTYPHIANEDEVNSSCRYLQRMVNLACVDALKVNVVYDIGNPKGIKCVRRGDVN 345

Query: 305 WKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLS 364
++FYD P + E Y Y H DKF DG+C+FWNCNVD YP N++VCR+DTR LS

Sbjct: 346 FRFYDKNPIVRNVKQFE---YDYNQHKDKFADGLCMFWNCNVDCYPDNSLVCRYDTRNLS 402

Query: 365 NLNLPGCDGGSlyVnKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVP 424
NLPGC+GGSlyVnKHAF+TP FD+ +F NLK +PFF+Y SPCE+ V+ D V

Sbjct: 403 VFNLPGCNGGSlyVnKHAFYTPKFDRISFRNLKAMPFFFYDSSPCETIQVDGVAQ-DLVS 461

Query: 425 LKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQ 484
L + CIT+CN+GGAVC+ HA Y +++ +YN ++AGF+ W+ + + YNLW +F+ LQ

Sbjct: 462 LATKDCITKCNIGGAVCKKHAQMYAEFVTSYNAAVTAGFTFWVTNKLNPYNLWKSFSALQ 521

>gi|9635157|ref|NP_058422.1| replicase [Transmissible gastroenteritis virus]

gi|7801348|emb|CAB91143.1| replicase [Transmissible gastroenteritis virus]

Length = 6685

Score = 545 bits (1403), Expect = e-153

Identities = 261/484 (53%), Positives = 335/484 (69%), Gaps = 13/484 (2%)

Query: 4 KDMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDVGTNLP 63
KD+ Y +IS MGF+ + GY +F TR+ A+R+VRAW+GFDVEG H D VGTN+P

Sbjct: 5574 KDVKYANVISYMGFRFEANIPGYHTLFCTRDFAMRNVRAWLGFDEGAHVCGDNVGTNVP 5633

Query: 64 LQLGFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRIKI 123
LQLGFS GV+ V G V TE V A+ PPG+QF HLIPLM KG PW++VR +I

Sbjct: 5634 LQLGFSNGVDFVVQTEGCVITEKGNSIEVVKARAPPGEQFAHLIPLMRKGQPWVHIVRRRI 5693

Query: 124 VQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIG-PERTCCLCDKRATCFSTSSDTYA 182
VQM+ D GLSD ++FVLWA G ELT+M+YFVKIG P++ C C K ATC+S+S YA

Sbjct: 5694 VQMVCDYFDGLSDILIFVLWAGGLELTMMRYFVKIGRPQK--CECGKSATCYSSSQSVYA 5751

Query: 183 CWNHSGVGFYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHEC 242
C+ H++G DY+YNP+ ID+QQWG+TG+L NH + C +H N HVAS DAIMTRCLA+H+C

Sbjct: 5752 CFKHALGCDYLYNPYCIDIQQWGYTGSLSMNHHEVCNIHRNEHVASGDAIMTRCLAIHDC 5811

Query: 243 FVKRVDWSVEYPIIGDELRVNSACRKVQHMVKSALLADKFPVLHDIGNPKAIKCVPAE 302
FVKRVDWS+ YP I +E ++N A R VQ V+K+AL +HD+GNPK I+C

Sbjct: 5812 FVKRVDWSIVYPFIDNEEKINKAGRIVQSHVMKAALKIFNPAAIHVDGNPKGIRCA-TTP 5870

Query: 303 VEWKFYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRV 362
+ W YD P ++ + L Y Y +H +G+ LFWNCNVD YP +IVCRFDTR

Sbjct: 5871 IPWFCYDRDPINN---NVRCLDYDYMVHGQ--MNGLMLFWNCNVDMYPEFSIVCRFDTRT 5925

Query: 363 LSNLNLPGCDGGSlyVnKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDY 422

S L+L GC+GG+LYVN HAFHTPA+D+ AF LK +PFFYY DS CE V +Y
 Sbjct: 5926 RSKLSLEGCNGGALYVNNHAFHTPAYDRRAFAKLKPMPPFFYYDDSNCE----LVDGQPNY
 5981

Query: 423 VPLKSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTR 482
 VPLKS CIT+CN+GGAVC+ HA YR Y++ YN+ + AGF++W + FDTY LW+ F
 Sbjct: 5982 VPLKSNVCITKCNIGGAVCKKHAALYRAYVEDYNI FMQAGFTIWCPQNFDTYMLWHGFVN
 6041

Query: 483 LQSL 486
 ++L
 Sbjct: 6042 SKAL 6045

>gi|19387582|ref|NP_598309.1| Pol1 [porcine epidemic diarrhea virus]
 gi|13752450|gb|AAK38661.1| Pol1 [porcine epidemic diarrhea virus]
 Length = 6781

Score = 541 bits (1394), Expect = e-152
 Identities = 256/480 (53%), Positives = 334/480 (69%), Gaps = 12/480 (2%)

Query: 8 YRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDVGTNLPLQLG 67
 Y +IS MGF+ + + + +F TR+ A+R+VR W+GFDVEG H VGTN+PLQLG
 Sbjct: 5675 YEHVISFMGFRFDINIPNHHTLFCTRDFAMRNVRGWLGFDFEGAHVVGSNVGTNVPLQLG
 5734

Query: 68 FSTGVNLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRKIVQML 127
 FS GV+ V P G V TE+ V A+ PPG+QF HL+PL+ +G PW+VVR +IVQM
 Sbjct: 5735 FSNGVDFVVRPEGCVVTESGDYIKPVRARAPPGEQFAHLLPLLKRGQPWDVVRKRIVQMC
 5794

Query: 128 SDTLKGLSDRVFVLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWNHS 187
 SD L LSD ++FVLWA G ELT+M+YFVKIGP ++C C K ATC++++ TY C+ H+
 Sbjct: 5795 SDYLANLSDILIFVLWAGGLELTTMRYFVKIGPSKSCD-CGKVATCYNSALHTYCCFKHA
 5853

Query: 188 VGFDYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVKRV 247
 +G DY+YNP+ ID+QQWG+ G+L NH +HC VH N HVAS DAIMTRCLA+H+CFVK V
 Sbjct: 5854 LGCDYLYNPYCIDIQQWGYKGSLSLNHHEHCNVHRNEHVASGDAIMTRCLAIHDCFVKNV
 5913

Query: 248 DWSVEYPIIGDELRVNSACRKVQHMVVKSAALLADKFPVLHDIGNPKAIKCVPAEVEWKF 307
 DWS+ YP IG+E +N + R VQ ++S L ++DIGNPK I+C + +W
 Sbjct: 5914 DWSITYPFIGNEAVINKSGRIVQSHTMRSVLKLYNPKAIYDIGNPKGIRCA-VTDAKWFC
 5972

Query: 308 YDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSNLN 367
 +D P + +E Y Y I H +F DG+CLFWNCNVDP ++VCRFDTR S LN
 Sbjct: 5973 FDKNPTNSNVKTL-----YDY-ITHGQF-DGLCLFWNCNVDMYPEFSVCRFDTRCRSPLN
 6027

Query: 368 LPGCDGGSlyVnKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSIDIDYVPLKS 427
 L GC+GGSlyVN HAFHTPAFDK AF LK +PFF+Y D+ C+ ++ I+YVPL++
 Sbjct: 6028 LEGCNGGSlyVNNHAFHTPAFDKRAFAKLKPMPPFFYYDDTECD----KLQDSINYVPLRA
 6083

Query: 428 ATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFT-RLQSL 486
 + CIT+CN+GGAVC H Y Y++AYN SAGF++W+ FDTYNLW TF+ LQ L
 Sbjct: 6084 SNCITKCNVGGAVCSKHCAMYHSYVNAYNTFTSAGFTIWWPTSFDTYNLWQTFSSNNLQGL
 6143

>gi|12175747|ref|NP_073549.1| replicase polyprotein lab [Human coronavirus
 229E]
 gi|12082740|gb|AAG48591.1|AF304460_2 replicase polyprotein lab [Human
 coronavirus 229E]
 Length = 6758

Score = 535 bits (1379), Expect = e-151
 Identities = 254/478 (53%), Positives = 329/478 (68%), Gaps = 13/478 (2%)

Query: 7 TYRRLISMGMGFKMNYQVNGYPNMFITREEAIRHVRWIGFDVEGCHATRDAVGTNLPLQL 66
 TY +IS MGF+ + + G ++F TR+ A+RHVR W+G DVEG H T D VGTN+PLQ+
 Sbjct: 5642 TYEHVISYMGFRFDVSMPSHSLFCTRDFAMRHVRGWLGMDEGAHVTDGNDVGTNVPLQV
 5701

Query: 67 GFSTGVNLVAVPTGYVDTENNTEFTRVNAKPPPGDQFKHLIPLMYKGLPWNVVRKIVQM 126
 GFS GV+ VA P G V T + V A+ PPG+QF H++PL+ KG PW+V+R +IVQM
 Sbjct: 5702 GFSNGVDFVAQPEGCVLTNTGSVVKPVRARAPPGEQFTHIVPLLRKGQPWSVLRKRIVQM
 5761

Query: 127 LSDTLKGLSDRVVFWLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYACWNH 186
 ++D L G SD +VFVLWA G ELT+M+YFVKIG + C C ATC+++ S+ Y C+ H
 Sbjct: 5762 IADFLAGSSDVLVFVLWAGGLELTTMRYFVKIGAVKH-CQCGTVATCYNVSNDYCCFKH
 5820

Query: 187 SVGFYVYNPFMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVKR 246
 ++G DYVYNP++ID+QQWG+ G+L +NH C VH N HVAS DAIMTRCLAV++CFVK
 Sbjct: 5821 ALGCDYVYNPYVIDIQQWGYVGSLSNHHAI CNVHRNEHVASGDAIMTRCLAVYDCFVK
 5880

Query: 247 VDWSVEYPIIGDELRVNSACRKYQHMVKSALLADKFPVLHDIGNPKAIKCPQAEVEWK 306
 VDWS+ YP+I +E +N R VQ ++++A+ +HDIGNPK I+C + +W
 Sbjct: 5881 VDWSITYPMIANENAINKGGRTVQSHIMRAAIKLYNPKAIHDIGNPKGIRCA-VTDAKWY
 5939

Query: 307 FYDAQPCSDKAYKIEELFYSAIHHDKFTDGVCLFWNCNVDRYPANAIVCRFDTRVLSNL 366
 YD P + +E Y Y H DG+CLFWNCNVDP YP +IVCRFDTR S L
 Sbjct: 5940 CYDKNPINSNVKTL---YDYMTHGQ--MDGLCLFWNCNVDMYPEFSIVCRFDTRTRSTL
 5994

Query: 367 NLPGCDGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYSDSPCESHGKQVVSID-IDYVPL 425
 NL G +GGSLYVN HAFHTPA+DK A LK PFFYY D CE VV D ++YVPL
 Sbjct: 5995 NLEGVNGGSLYVNNHAFHTPAYDKRAMAKLPAPFFYYDDGSCE-----VVHDQVNYVPL
 6049

Query: 426 KSATCITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRL 483
 ++ CIT+CN+GGAVC HAN YR Y+++YN+ AGF++W+ FD YNLW TFT +
 Sbjct: 6050 RATNCITKCNIGGAVCSKHANLYRAYVESYNIFTQAGFNIWVPTTFDCYNLWQTFTEV 6107

>gi|133591|sp|P18458|RRPB_BEV RNA-directed RNA polymerase (ORF1B)
 gi|94017|pir||S11238 polymerase - Berne virus
 gi|1334814|emb|CAA36601.1| 2nd polymerase reading frame (AA 1-2291)
 [Berne virus]

Length = 2291

Score = 50.1 bits (118), Expect = 8e-05

Identities = 37/103 (35%), Positives = 54/103 (52%), Gaps = 11/103 (10%)

Query: 140 FVLWAHGFELTSMKYFVKIGPERTC--CLCDKRATCFSTSSDTYACWNHSGVF--DYVYN 195
 F+L++ +L S+K++V+ TC C C + A C + Y C N G + N
 Sbjct: 1511 FILYSCSNDLKSLKFYVEFD---TCYFCSCGEMAICLMRDGN-YKCRNCYGGMLISKLVN
 1566

Query: 196 PFMIDVQQWGFTGNLQSNHDQHC-QVHGNAHVASCDAIMTRCL 237

+DVQ+ LQ HD C Q HG++H A CDA+MT+CL

Sbjct: 1567 CKYLDVQKERV--KLQDAHDAICQQFHGDSHEALCDAVMTKCL 1607

>gi|1513061|dbj|BAA13323.1| cyanoprotein alpha subunit precursor
 [Riptortus clavatus]

Length = 693

Score = 34.7 bits (78), Expect = 3.7

Identities = 16/36 (44%), Positives = 22/36 (61%), Gaps = 1/36 (2%)

Query: 371 CDGGS LYVNKHAFTPAFDKSAFTNLKQLPFFYYSD 406

C G LY +KHA P FD+ A+ + Q+P FY+ D

Sbjct: 643 CGGSKLYDSKHAMGFP-FDRPAYPDAFQVPNFYFKD 677

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF

Posted date: Apr 11, 2003 2:30 AM

Number of letters in database: 454,141,287

Number of sequences in database: 1,411,415

Lambda	K	H
0.325	0.139	0.456

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 473,361,261

Number of Sequences: 1411415

Number of extensions: 20503315

Number of successful extensions: 51018

Number of sequences better than 10.0: 27

Number of HSP's better than 10.0 without gapping: 26

Number of HSP's successfully gapped in prelim test: 1

Number of HSP's that attempted gapping in prelim test: 50937
Number of HSP's gapped (non-prelim): 33
length of query: 486
length of database: 454,141,287
effective HSP length: 127
effective length of query: 359
effective length of database: 274,891,582
effective search space: 98686077938
effective search space used: 98686077938
T: 11
A: 40
X1: 15 (7.0 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (21.6 bits)
S2: 75 (33.5 bits)

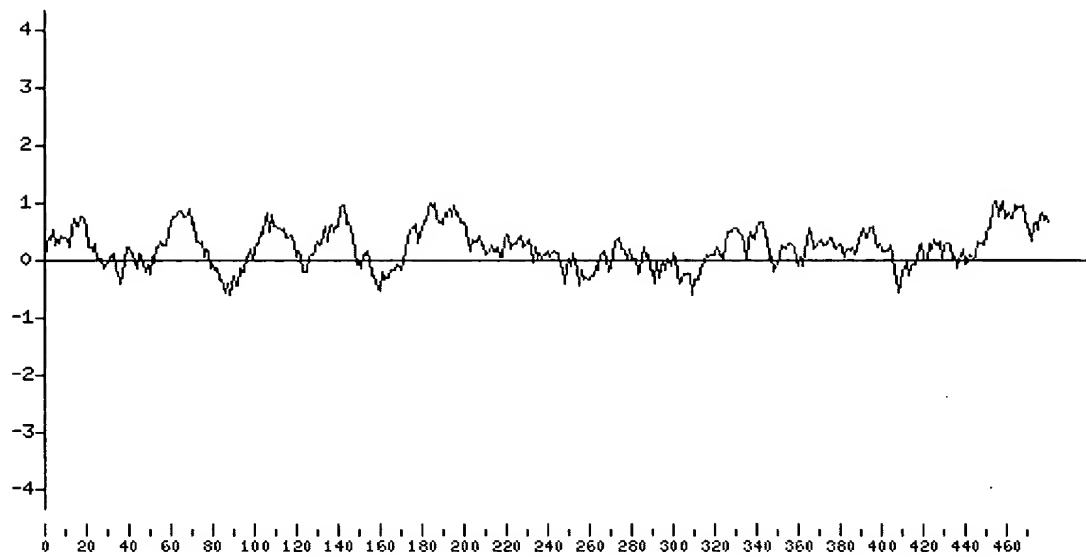
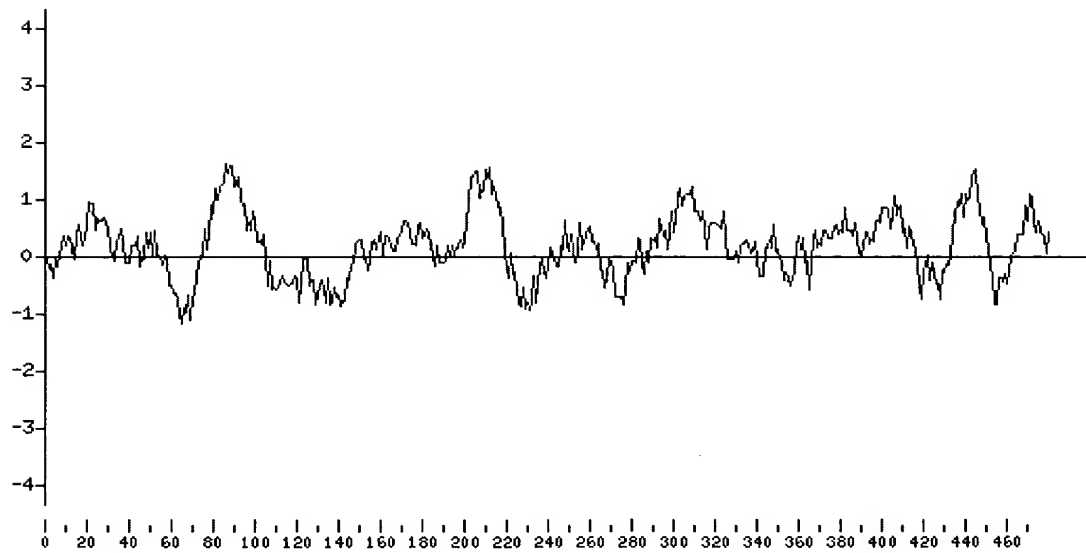
FIGURE 125**FIGURE 125A****FIGURE 125B**

FIGURE 126**5'3' Frame 1**

QVHQNVCVL-LIFYLMTLSR--SHKICQ-FQKWSRLQLTMLKFHSCFGVRMDMLKPSTQN
YKQVKRGNQVLRCLCTRCCKEFLKSVTFRIMVKMLLYQKE---MSQSILNCVNT-IHLL
-LYPPT-ELFTLV

5'3' Frame 2

RFIKMCVFCD-SFT--LCRDNKVTRFVSDFKSGQGYN-LC-NFIHALV-GWTC-NLLPKT
TSKSSVATRCCDA-LVQDAKNAS-KV-PSELW-KCCYTKRNNDECRKVYSTVSILKYTYF
SCTLQHESYSLWCW

5'3' Frame 3

GSSKCVCSVIDLLDDFVEIIKSQDLSVISKVVKVTIDYAEISFMLWCKDGHVETFYPKL
QASQAWQPGVAMPNLYKMQRMLLEKCDLQNYGENAVIPKGIMMNVAKYTQLCQYLNTLTL
AVPSNMRVIHFGAG

3'5' Frame 1

PAPK-ITLMLEGTAKVSVFKY-HS-VYFATFIIIPFGITAFSP-F-RSHFSRSILCILYK
LGIATPGCHA-LACSGF-KVSTCPSLHQSMNEISA-SIVTLTTFEITDKSCDFIISTKSS
SKRSITEHTHFDEP

3'5' Frame 2

QHQSE-LSCWRVQLK-VYLSIDTVEYTLRHSSLFLLV-QHFHHNSEGHTFQEAFASCTS
-ASQHLVATLDLLVVLGRRFQHVHPYTKA-MKFQHSQ-L-P-PLLKSLTNLVTLRSRQSHQ
VKDQSQNTHILMNL

3'5' Frame 3

STKVNNSHVGGYS-SKCI-VLTQLSILCDIHHSFWYNSIFTIILKVTLFKKHSLLHVQV
RHRNTWLPRLTCL-FWVEGFNMSILTPKHE-NFSIVNCNLDHF-NH-QIL-LYYLDKVIK
-KINHRHTFT-T

FIGURE 127**5'3' Frame 1**

-VFTYPGKANQPRSLVDLFSKRTN-NV--WTPIKPT-CPPHYIWWTHRFN-Q-PEWRTAM
GQGQNSADPKVYPIILRLGSQLSLSMARRNLDSEARAFQSTPIVVQMTKLATTEELPDE
FVVVTAK-KSSAPDGTSIT-ELAQKLHFPTALTKKASYGLQLREP-IHPKTTLAPAILIT
MLPPCYNFLKEQHCQKASTQREAEAAVKPLLAPHHVVAVIQEIQLLA AVGEILLLEWLAE
VVKLPSRYCC-TD-TSLRAKFLVKANNKAKLSLRNLLLRHLKSLAKNVLPQNSTTSLKH
LGDVVQNKPKKEISGTKT-SDKELITNIGPQIAQFA

5'3' Frame 2

RFLPTQEKPNTDLL-ICSLNEQIKMSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGLQW
GKAKTAPTFRFTQ-YCVLVHSSSAWQGGT-IPSRPGRSNQHQ-WSR-PNWLLPKSYPTS
SWW-RQNERAQPMVLLLPRNWPRSFTSLRR-QRRHRMGCN-GSLEYTORPHWHPQS--Q
CCHRATTSSRNIAKRLLRGKQRRQSSLESLLIT-SR-FKKFNSWQQ-GKFSCSNG-RR
W-NCPRAIARQIEPA-EQSFW-RPTTTRPNCH-EICC-GI-KASPKTYCHKTVQRHSSI
WETWSRTNPRKFRGPRPNQTRN-LQTLGRKLHNL

5'3' Frame 3

GFYLPKRSQPTSISCRSVL-TNKLKCLIMDPNQTNVVPALHLVDPQIQLTITRMEDCNG
ARPKQRRPQGLPNNIASWFTALTQHGKEELRFPRGQGVPIINTNSGPDDQIGYYRRARRV
RGGDGKMKELSPRWYFYLLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNN
AATVLQLPQGTTLPKGFYAEGSRGGSQASSRSSRSRGNSTPGSSRGNSPARMASGG
GETALALLLLDRLNQLESKVSGKGQQQOGQTVTKKSAAEASKKPRQKRTATKQYNVTQAF
GRRGPEQTQGNFGDQDLIRQGTQDYKHWAACTIC

3'5' Frame 1

RQIVQFAAQCL-SVPCLIRSWSPKFPWVCSGPRLPNA-VTLYCFVAVRFWRGFLDASAAD
FLVTVPCCCWPLPETLLSSWFNLSSSNSARAVSPPPLAIRAGEFPLLLPGVEFLELPRL
RDEEREEA-LPPLLPSA-KPFGNVVP-GSCSTVAALLGLRVPMWSLGVFKAPSVATHM
PSLLAP-GSEASGPVPR--KYHLGLSSFILPSPRTRRVALR--PIWSSGPLLVLIGTPW
PRGNLSSSLPC-VRAVNQDAILLGKPWGRRCFGLAPLQSSILVIVS-ICGSTKCNAGGTT
LV-LGSIIRHFNLFV-RTDLQEIEVGWLFGLGR-KP

3'5' Frame 2

GKLCNLRPNVCNQFLV-LGLGPRNFLGFVLDHVSQMLE-RCTVLWQYVFGAEF-MPQQQI

S--QFGLVVVGLYQKLCSQAGSICLAAIARGQFHHLR-PFEQENFPYCCQELNFLNYRDY
 VMRSEKRLDCRLCFPLRRSLLAMLFLEEVVARWQHGY-DCGCQCGLWVYSRLPQLQPIRC
 LLC-RRREVKLLGQFLGNRSTIWG-ALSFCRHHHELVG-LFGSSQFGHLDHYWC-LERPG
 LEGI-VPPCHAE-EL-TKTQYYWVNLGVGAVLALPHCSPPFWLLSVESVGPPNVMRGALR
 WFDWGPLSDILICSFREQIYKRSRLVGFSWVGKNL

3'5' Frame 3

ANCAICGPMFVISSLSD-VLVPEISLGLFWTTSPKCLSDVVLFCGSTFLARLFRCLSSRF
 LSDSLALLLLAFTRNFAKLVSQSV-QQ-REGSFTTSASHSSRRISPTAARS-IS-ITATT
 --GARRGLTAASASLCVEAFWQCCSLRKL-HGGSIVIRIAGANVVFVFCIQGSLSCNPYDA
 FFFSAVGK-SFWASS-VIEVPSGAELFHFAVTTTNSGSSSVVANLVIWTTIGVDWNALA
 SRESKFLAMLSESCPEPRNIIG-TLGSALFWPCPIAVLHSGYCQLNLWVHQM-CGGHYV
 GLIGVHYQTF-FVRLNRSTRDRGWLAFFPG-VKT

FIGURE 128

-GLELKL-LTSICAF-PFCYSLF--CLLYFGFHKSRI-KNLVPKSKRT-NFSLF-LVFL
 YAVAYAL-YSAVHLINLMCLKILVRYNTRGNTYSTAWLCALGKVLPHRWHTMVQTCTPN
 VTINCQDPAGGALIARCWYLHEGHQTAAFRDVLVVLNKRNT-NV--WTPIKPT-CPPHYI
 WWTHRFN-Q-PEWRTQWGKAKTAPTFRFTQ-YCVLVHSSHSAWQGGT-IPSRPGRSNQHQ
 -WSR-PNWLLPKSYPTSSWW-RQNERAQPMVLLLPRNWPRSFTSLRR-QRRHRMGCN-G
 SLEYTQRPWHHPQS--QCCHRATTSSRNNAKRLLRGKQRRQSSLSLLIT-SR-FKKF
 NSWQQ-GKFSCSNG-RRW-NCPRAAARQIEPA-EQSEW-RPTTTRPNCH-EICC-GI-K
 ASPKTYCHKTQVRHSSIWETWSRTNPRKFRGPRPNQTRN-LQTLAANCTICKKCLCILWN
 VTHWHGSHTFGNMADLSWSH-IG-QRSTIQQRHTAEQAH-RIQNIPTNRA-KGQKEKD-
 -SSAFAAETKEAAHCDSSSC

EDSSSSFN-LLFVLFSLSAIPCFNNAYYILVFTRNPGSRRTLYQSLNEHETSHCFDLYFS
 MQLHMHCTALCI--TSCA-RSL-GTTGLVILIALLGFL-ERFYLFIDGTLWFKHAHLM
 LLSTVKIQLVVRL-LGVGTFMKVTKLLHLETYLLF-INEQIKMSDNGPQSNQRSAPRITF
 GGPTDSTDNNQNGGRNGARPKQRRPQGLPNNIASWFTALTQHGKEELRFPRGQGVPIINTN
 SGPDDQIGYYRRATRRVRGGDGKMKELSPRWYFYLLGTGPEASLPYGANKEGIVWVATEG
 ALNTPKDHIGTRNPNNNAATVLQLPQGTTLPGFYAEGSRGGSQASSRSSSRSGNSRNS
 TPGSSRGNSPARMASGGGETALALLLLDRLNQLESKVSQGGQGGQTVTKKSAAEASKK
 PRQKRTATKQYNVTQAFGRGPEQTQGNFGDQDLIRQGTQDYKHWPQIAQFAPSASAFFGM
 SRIGMEVTPSGTWLTYHGAIKLDDKDPQFKDNVILLNKHIDAYKTFPPTPKDKKKKTD
 EAQPLPQRQKKQPTVTLLP

RTRAQALIDFYLCFLAFLFLVLIMLIIFWFSLEIQDLEEPCTKV-TNMKLLIVLTCISL
 CSCICTVQRCASNKPHVLEDPCVKQH-G-YL-HCLALCSRKGFTFS-MAHYGSNMHT-C
 YYQLSRSSWWCAYS-VLVPS-RSPNCCI-RRTCCFK-TNKLKCLIMDPNQTNVVPALHL
 VDPQIQLTITRMEDAMGQGQNSADPKVYPIILRLGSQSLSMARRNLDSEARAFQSTPI
 VVQMTKLATTEELPDEFVVVTAK-KSSAPDGTSIT-ELAQKLHFPTALTKKASYGLQRE
 P-IHPKTTLAPAILITMLPPCYNFLKEQHCQKASTQREAEAAVKPLLAPHHVVAVIQEIQ
 LLAAVGEILLLEWLAEVVKLPSRYCC-TD-TSLRAKFLVKANNKAKLSLRNLLLRHLKS
 LAKNVLPQNSTTSLKHLGDVVQNKPKKEISGTKT-SDKELITNIGRKLHNLLQVPLHSLEC
 HALAWKSHLREHG-LIMEPLNWMTKIHNSKTTSYC-TSTLTHTKHSQQSLKRTKRKRLM
 KLSLCRRDKRSSPL-LFFL

FIGURE 129

5'3' Frame 1

taccgtagactcatctctatgatgggtttcaaaatgaattaccaagtcaatgggttacct
 Y R R L I S M M G F K M N Y Q V N G Y P
 aatatgtttatcacccgcgaagaagctattcggtcacgttcgtgcgtggattggctttgat
 N M F I T R E E A I R H V R A W I G F D
 gtagagggctgtcatgcaactagagatgctgtgggtactaacctacctctccagctagga
 V E G C H A T R D A V G T N L P L Q L G
 ttttctacaggtgttaacttagtagctgtaccgactgggttatgttgacactgaaaataac
 F S T G V N L V A V P T G Y V D T E N N
 acagaattcaccagagttaatgcaaaacctccaccaggtgaccagtttaaacatcttatacc
 T E F T R V N A K P P P G D Q F K H L I

5'3' Frame 2

taccgtagactcatctctatgatgggtttcaaaatgaattaccaagtcaatgggttaccta
 T V D S S L - W V S K - I T K S M V T L
 atatatgtttatcacccgcgaagaagctattcggtcacgttcgtgcgtggattggctttgatg
 I C L S P A K K L F V T F V R G L A L M
 tagagggctgtcatgcaactagagatgctgtgggtactaacctacctctccagctaggat
 - R A V M Q L E M L W V L T Y L S S - D
 ttttctacaggtgttaacttagtagctgtaccgactgggttatgttgacactgaaaataaca
 F L Q V L T - - L Y R L V M L T L K I T
 cagaattcaccagagttaatgcaaaacctccaccaggtgaccagtttaaacatcttatacc
 Q N S P E L M Q N L H Q V T S L N I L Y

5'3' Frame 3

taccgtagactcatctctatgatgggtttcaaaatgaattaccaagtcaatgggttaccctaa
P - T H L Y D G F Q N E L P S Q W L P -
tatgtttatcacccgcgaagaagctattcgtcacgttcgtgctggattggctttgatgt
Y V Y H P R R S Y S S R S C V D W L - C
agagggctgtcatgcaactagagatgctgtgggtactaacctacctctccagctaggatt
R G L S C N - R C C G Y - P T S P A R I
ttctacaggtgttaacttagtagctgtaccgactgggttatgttgacactgaaaataacac
F Y R C - L S S C T D W L C - H - K - H
agaattcaccagagttaatgcaaaacctccaccaggtgaccagtttaaacatcttataacc
R I H Q S - C K T S T R - P V - T S Y T

3'5' Frame 1

gggtataagatgttttaaactgggtcacctgggtggaggttttgcattaactctggtgaattct
G I R C L N W S P G G G F A L T L V N S
gtgttattttcagtggtcaacataaccagtcggtacagctactaagttaacacctgtagaa
V L F S V S T - P V G T A T K L T P V E
aatcctagctggagaggttaggttagtaccacagcatctctagttgcatgacagccctct
N P S W R G R L V P T A S L V A - Q P S
acatcaaagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacata
T S K P I H A R T - R I A S S R V I N I
ttagggtaaccattgacttggttaattcattttgaaacccatcatagagatgagtctacggta
L G - P L T W - F I L K P I I E M S L R

3'5' Frame 2

gggtataagatgttttaaactgggtcacctgggtggaggttttgcattaactctggtgaattctg
V - D V - T G H L V E V L H - L W - I L
tggttattttcagtggtcaacataaccagtcggtacagctactaagttaacacctgtagaaa
C Y F Q C Q H N Q S V Q L L S - H L - K
atcctagctggagaggttaggttagtaccacagcatctctagttgcatgacagccctcta
I L A G E V G - Y P Q H L - L H D S P L
catcaaagccaatccacgcacgaacgtgacgaatagcttcttcgcgggtgataaacatat
H Q S Q S T H E R D E - L L R G - - T Y
tagggtaaccattgacttggttaattcattttgaaacccatcatagagatgagtctacggta
- G N H - L G N S F - N P S - R - V Y G

3'5' Frame 3

ggtataagatgttttaaactggtcacctgggtggaggttttgcattaactctggtgaattctgt
 Y K M F K L V T W W R F C I N S G E F C
 gttattttcagtggtcaacataaccagtcggtacagctactaagttaacacctgtagaaaa
 V I F S V N I T S R Y S Y - V N T C R K
 tcctagctggagaggttaggttagtacccacagcatctctagttgcatgacagccctctac
 S - L E R - V S T H S I S S C M T A L Y
 atcaaagccaatccacgcacgaacgtgacgaatagcttcttcgcggtgataaacatatt
 I K A N P R T N V T N S F F A G D K H I
 agggtaaccattgacttggttaattcattttgaaacccatcatagagatgagtctacggta
 R V T I D L V I H F E T H H R D E S T V

FIGURE 130

	10	20	30	40	50	60
SEQ ID NO: 9997	KGHDLRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLP					
SEQ ID NO:10034	----YRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLP					

Prim. Cons.	KGHD2RRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGCHATRDAVGTNLP					

	70	80	90	100	110	120
SEQ ID NO: 9997	LQLGFSTGVNVLVAVPTGYVDTENNTKFTRVNAQTSTSEQFKHLIPLMYKGLPWNVVRKI					
SEQ ID NO:10034	LQLGFSTGVNVLVAVPTGYVDTENNTFTRVNAKPPPGDQFKHLI-----					
	*****:*****:.....:*****					
Prim. cons.	LQLGFSTGVNVLVAVPTGYVDTENNT2FTRVNA22222QFKHLIPLMYKGLPWNVVRKI					

	130	140	150	160	170	180
SEQ ID NO: 9997	VQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYAC					
SEQ ID NO:10034	-----					

Prim. cons.	VQMLSDTLKGLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDKRATCFSTSSDTYAC					
-------------	---	--	--	--	--	--

	190	200
SEQ ID NO: 9997	WNHVGFDYVYNPFMIDVQQWGLYG	
SEQ ID NO:10034	-----	

FIGURE 131**5'3' Frame 1**

caggttcatcaaaaatgtgtgtgttctgtgattgatcttttacttgatgactttgtcgaga
 Q V H Q N V C V L - L I F Y L M T L S R
 taataaagtcacaagatttgtcagtgatttcaaaagtgggtcaaggttacaattgactatg
 - - S H K I C Q - F Q K W S R L Q L T M
 ctgaaatttcattcatgctttggtgtaaggatggacatggtgaaaccttctacccaaaac
 L K F H S C F G V R M D M L K P S T Q N
 tacaagcaagtcaagcgtggcaaccaggtgttgcgatgcctaacttgataagatgcaaa
 Y K Q V K R G N Q V L R C L T C T R C K
 gaatgcttcttgaaaagtgtgaccttcagaattatggtgaaaatgctgttatacaaaaag
 E C F L K S V T F R I M V K M L L Y Q K
 gaataatgatgaatgtcgcaaagtataactcaactgtgtcaataacttaatacacttactt
 E - - - M S Q S I L N C V N T - I H L L
 tagctgtaccctccaacatgagagttattcactttggtgctgg
 - L Y P P T - E L F T L V L

5'3' Frame 2

caggttcatcaaaaatgtgtgtgttctgtgattgatcttttacttgatgactttgtcgagat
 R F I K M C V F C D - S F T - - L C R D
 aataaagtcacaagatttgtcagtgatttcaaaagtgggtcaaggttacaattgactatgc
 N K V T R F V S D F K S G Q G Y N - L C
 tgaaatttcattcatgctttggtgtaaggatggacatggtgaaaccttctacccaaaact
 - N F I H A L V - G W T C - N L L P K T
 acaagcaagtcaagcgtggcaaccaggtgttgcgatgcctaacttgataagatgcaaa
 T S K S S V A T R C C D A - L V Q D A K
 aatgcttcttgaaaagtgtgaccttcagaattatggtgaaaatgctgttatacaaaaag
 N A S - K V - P S E L W - K C C Y T K R
 aataatgatgaatgtcgcaaagtataactcaactgtgtcaataacttaatacacttacttt
 N N D E C R K V Y S T V S I L K Y T Y F
 agctgtaccctccaacatgagagttattcactttggtgctgg
 S C T L Q H E S Y S L W C W

5'3' Frame 3

caggttcatcaaaaatgtgtgtgttctgtgattgatcttttacttgatgactttgtcgagata
 G S S K C V C S V I D L L L D D F V E I
 ataaagtcacaagatttgtcagtgatttcaaaagtgggtcaaggttacaattgactatgct
 I K S Q D L S V I S K V V K V T I D Y A
 gaaatttcattcatgctttggtgtaaggatggacatggtgaaaccttctacccaaaacta
 E I S F M L W C K D G H V E T F Y P K L
 caagcaagtcaagcgtggcaaccaggtgttgcgatgcctaacttgataagatgcaaa
 Q A S Q A W Q P G V A M P N L Y K M Q R

191/199

atgcttcttgaaaagtgtgaccttcagaattatgggtgaaaatgctgttataccaaaaagga
 M L L E K C D L Q N Y G E N A V I P K G
 ataatgatgaatgtcgcgcaaagtataactcaactgtgtcaataacttaaatacacttacttta
 I M M N V A K Y T Q L C Q Y L N T L T L
 gctgtaccctccaacatgagagttattcacttttggtgctgg
 A V P S N M R V I H F G A

3'5' Frame 1

ccagcaccaaagtgaataactctcatggttgagggtacagctaaagtaagtgtatttaag
 P A P K - I T L M L E G T A K V S V F K
 tattgacacagttgagtatactttgcgacattcatcattattccttttggtataacagca
 Y - H S - V Y F A T F I I I P F G I T A
 ttttcaccataattctgaaggtcacacttttcaagaagcattcctttgcatcttgtacaag
 F S P - F - R S H F S R S I L C I L Y K
 ttaggcacgcgaacacctggttgccacgcttgacttgcttgtagttttgggtagaagggtt
 L G I A T P G C H A - L A C S F G - K V
 tcaacatgtccatccttacaccaaagcatgaatgaaatttcagcatagtcaattgtaacc
 S T C P S L H Q S M N E I S A - S I V T
 ttgaccacttttgaaatcactgacaaatcttgtgactttattatctcgacaaagtcacaa
 L T T F E I T D K S C D F I I S T K S S
 agtaaaagatcaatcacagaacacacacattttgatgaacctg
 S K R S I T E H T H F D E P

3'5' Frame 2

ccagcaccaaagtgaataactctcatggttgagggtacagctaaagtaagtgtatttaagt
 Q H Q S E - L S C W R V Q L K - V Y L S
 attgacacagttgagtatactttgcgacattcatcattattccttttggtataacagcat
 I D T V E Y T L R H S S L F L L V - Q H
 ttttcaccataattctgaaggtcacacttttcaagaagcattcctttgcatcttgtacaagt
 F H H N S E G H T F Q E A F F A S C T S
 taggcacgcgaacacctggttgccacgcttgacttgcttgtagttttgggtagaagggtt
 - A S Q H L V A T L D L L V V L G R R F
 caacatgtccatccttacaccaaagcatgaatgaaatttcagcatagtcaattgtaacct
 Q H V H P Y T K A - M K F Q H S Q L - P
 tgaccacttttgaaatcactgacaaatcttgtgactttattatctcgacaaagtcacaa
 - P L L K S L T N L V T L L S R Q S H Q
 gtaaaagatcaatcacagaacacacacattttgatgaacctg
 V K D Q S Q N T H I L M N L

3'5' Frame 3

ccagcaccaaagtgaataactctcatggttgagggtacagctaaagtaagtgtatttaagta
 S T K V N N S H V G G Y S - S K C I - V

ttgacacagttgagtatactttgcgacattcatcattattccttttgggtataacagcatt
 L T Q L S I L C D I H H Y S F W Y N S I
 ttcaccataattctgaaggtcacacttttcaagaagcattctttgcatcttgtacaagtt
 F T I I L K V T L F K K H S L H L V Q V
 aggcacgcgaacacctgggtgccacgcttgacttgctttagttagtttgggtagaaggtttc
 R H R N T W L P R L T C L - F W V E G F
 aacatgtccatccttacaccaagcatgaatgaaatttcagcatagtcaattgtaacctt
 N M S I L T P K H E - N F S I V N C N L
 gaccacttttgaatcactgacaaatcttgtga'ctttattatctcgacaaagtcataag
 D H F - N H - Q I L - L Y Y L D K V I K
 taaaagatcaatcacagaacacacacattttgatgaacctg
 - K I N H R T H T F - - T

FIGURE 132

5'3' Frame 1

taggtttttacctaaccaggaagccaaacacctcgatctctttagatctgttctct
 - V F T Y P G K A N Q P R S L V D L F S
 aaacgaacaaattaaaatgtctgataatggacccaatcaaaccaacgtagtgcccccg
 K R T N - N V - - W T P I K P T - C P P
 cattacatttgggtggaccacagattcaactgacaataaccagaatggaggactgcaatg
 H Y I W W T H R F N - Q - P E W R T A M
 gggcaaggccaaaacagcgccgacccaaggtttaccaataatattgcttcttgggttca
 G Q G Q N S A D P K V Y P I I L R L G S
 cagctctcactcagcatggcaaggaggaacttagattccctcgaggccaggcggttccaa
 Q L S L S M A R R N L D S L E A R A F Q
 tcaacaccaatagtggtccagatgaccaaattggctactaccgaagagctacccgacgag
 S T P I V V Q M T K L A T T E E L P D E
 ttcgtgggtggtagcggaatgaaagagctcagccccagatggtagtcttctattacctag
 F V V V T A K - K S S A P D G T S I T -
 gaactggcccagaagcttcacttccctacggcgctaacaaagaaggcatcgtaggggttg
 E L A Q K L H F P T A L T K K A S Y G L
 caactgagggagccttgaatacacccaaagaccacattggcaccgcgaatcctaataaca
 Q L R E P - I H P K T T L A P A I L I T
 atgctgccaccgtgctacaacttccctcaaggaacaacattgccaaaaggcttctacgcag
 M L P P C Y N F L K E Q H C Q K A S T Q
 agggaagcagaggcggcagtcagcctcttctcgtcctcatcacgtagtcgcggttaatt
 R E A E A A V K P L L A P H H V V A V I
 caagaaattcaactcctggcagcagtaggggaaattctcctgctcgaatggctagcggag
 Q E I Q L L A A V G E I L L L E W L A E
 gtgggtgaaactgccctcgcgctattgctgctagacagattgaaccagcttgagagcaaag
 V V K L P S R Y C C - T D - T S L R A K
 tttctgggtaaaggccaacaacaagaaggccaaactgtcactaagaaatctgctgctgagg

193/199

F L V K A N N N K A K L S L R N L L L R
 catctaaaaagcctcgccaaaaacgtactgccacaaaacagtacaacgtcactcaagcat
 H L K S L A K N V L P Q N S T T S L K H
 ttgggagacgtggtccagaacaaacccaaggaaatttcggggaccaagacctaatcagac
 L G D V V Q N K P K E I S G T K T - S D
 aaggaaactgattacaaacattggggccgcaaattgcacaatttgcct
 K E L I T N I G P Q I A Q F A

5'3' Frame 2

taggtttttacctaccaggaagccaaacacctcgatctctttagatctgttctcta
 R F L P T Q E K P T N L D L L - I C S L
 aacgaacaaattaaaatgtctgataatggacccaatcaaaccaacgtagtgtccccgc
 N E Q I K M S D N G P Q S N Q R S A P R
 attacatttgggtggaccacagattcaactgacaataaccagaatggaggactgcaatgg
 I T F G G P T D S T D N N Q N G G L Q W
 ggcaaggccaaaaacagcgccgacccaagggtttaccaataatattgctgttgggtcac
 G K A K T A P T P R F T Q - Y C V L V H
 agctctcactcagcatggcaaggaggaacttagattccctcgaggccagggcggttccaat
 S S H S A W Q G G T - I P S R P G R S N
 caacaccaatagtgttcagatgaccaaattggctactaccgaagagctacccgacgagt
 Q H Q - W S R - P N W L L P K S Y P T S
 tcgtggtggtgacggcaaaatgaaagagctcagccccagatggtacttctattacctagg
 S W W - R Q N E R A Q P Q M V L L L P R
 aactggcccagaagcttcacttccctacggcgctaacaagaaggcatcgtagtgggttgc
 N W P R S F T S L R R - Q R R H R M G C
 aactgagggagccttgaatacacccaaagaccacattggcaccgcaatcctaataacaa
 N - G S L E Y T Q R P H W H P Q S - - Q
 tgctgccaccgtgctacaacttccctcaaggaacaacattgccaaaaggcttctacgcaga
 C C H R A T T S S R N N I A K R L L R R
 ggaagcagagggcggcagtcagcctcttctcgctcctcatcacgtagtcgcggtaatc
 G K Q R R Q S S L F S L L I T - S R - F
 aagaaattcaactcctggcagcagtaggggaaattctcctgctcgaatggctagcggagg
 K K F N S W Q Q - G K F S C S N G - R R
 tgggtgaaactgccctcgcgctattgctgctagacagattgaaccagcttgagagcaaagt
 W - N C P R A I A A R Q I E P A - E Q S
 ttctggttaaaggccaacaacaagaaggccaaactgtcactaagaaatctgctgctgaggc
 F W - R P T T T R P N C H - E I C C - G
 atctaaaaagcctcgccaaaaacgtactgccacaaaacagtacaacgtcactcaagcatt
 I - K A S P K T Y C H K T V Q R H S S I
 tgggagacgtggtccagaacaaacccaaggaaatttcggggaccaagacctaatcagaca
 W E T W S R T N P R K F R G P R P N Q T
 aggaactgattacaaacattggggccgcaaattgcacaatttgcct
 R N - L Q T L G R K L H N L P

5'3' Frame 3

taggtttttacctacccaggaaaagccaaccaacctcgatctctttagtagatctgttctctaa
 G F Y L P R K S Q P T S I S C R S V L -
 acgaacaaattaaaaatgtctgataatggaccccaatcaaaccaacgtagtgcccccgca
 T N K L K C L I M D P N Q T N V V P P A
 ttacatttggtggacccacagattcaactgacaataaccagaatggaggactgcaatggg
 L H L V D P Q I Q L T I T R M E D C N G
 gcaaggccaaaacagcgccgaccccaaggtttacccaataatattgcgtcttggttcaca
 A R P K Q R R P Q G L P N N I A S W F T
 gctctcactcagcatggcaaggaggaacttagattccctcgaggccaggcggttccaatc
 A L T Q H G K E E L R F P R G Q G V P I
 aacaccaatagtggtccagatgaccaaattggctactaccgaagagctacccgacgagtt
 N T N S G P D D Q I G Y Y R R A T R R V
 cgtggtggtgacggcaaaatgaaagagctcagccccagatgggtacttctattacctagga
 R G G D G K M K E L S P R W Y F Y Y L G
 actggcccagaagcttcacttccctacggcgctaacaagaaggcatcgtaggggttgca
 T G P E A S L P Y G A N K E G I V W V A
 actgagggagccttgaatacacccaaagaccacattggcaccgcgaatcctaataacaat
 T E G A L N T P K D H I G T R N P N N N
 gctgccaccgtgctacaacttccctcaaggaacaacattgccaaaaggcttctacgcagag
 A A T V L Q L P Q G T T L P K G F Y A E
 ggaagcagaggcggcagtcagcctcttctcgctcctcatcacgtagtcgcggttaattca
 G S R G G S Q A S S R S S S R S R G N S
 agaaattcaactcctggcagcagtaggggaaatttctcctgctcgaatggctagcggaggt
 R N S T P G S S R G N S P A R M A S G G
 ggtgaaactgccctcgcgctattgctgctagacagattgaaccagcttgagagcaaagtt
 G E T A L A L L L L D R L N Q L E S K V
 tctggtaaaggccaacaacaacaaggccaaactgtcactaagaaatctgctgctgaggga
 S G K G Q Q Q Q G Q T V T K K S A A E A
 tctaaaaagcctcgccaaaaacgtactgccacaaaacagtacaacgtcactcaagcattt
 S K K P R Q K R T A T K Q Y N V T Q A F
 gggagacgtggtccagaacaaacccaaggaaatttcggggaccaagacctaatcagacaa
 G R R G P E Q T Q G N F G D Q D L I R Q
 ggaactgattacaaacattgggccgcaaattgcacaatttgct
 G T D Y K H W A A N C T I C

3'5' Frame 1

aggcaaattgtgcaatttgcggcccaatgtttgtaatcagttccttgtctgattaggtct
 R Q I V Q F A A Q C L - S V P C L I R S
 tggccccgaaatttcccttgggtttgttctggaccacgtctcccaaattgcttgagtgcg
 W S P K F P W V C S G P R L P N A - V T
 ttgtactgttttgtggcagtagctttttggcgaggcttttttagatgcctcagcagcagat
 L Y C F V A V R F W R G F L D A S A A D
 ttcttagtgacagtttggccttgttgttgttggcctttaccagaaactttgctctcaagc
 F L V T V W P C C C W P L P E T L L S S
 tggttcaatctgtctagcagcaatagcgcgagggcagtttcaccacctccgctagccatt

W F N L S S S N S A R A V S P P P L A I
 cgagcaggagaatttcccctactgctgccaggagttgaatttcttgaattaccgcgacta
 R A G E F P L L L P G V E F L E L P R L
 cgtgatgaggagcgagaagaggcttgactgccgcctctgcttccctctgcgtagaagcct
 R D E E R E E A - L P P L L P S A - K P
 tttggcaatgttgttccttgaggaagttgtagcacggtggcagcattgttattaggattg
 F G N V V P - G S C S T V A A L L L G L
 cgggtgccaatgtggtctttgggtgtattcaaggctccctcagttgcaaccatacga
 R V P M W S L G V F K A P S V A T H T M
 ccttctttgttagcgccgtagggaagtgaagcttctgggccagttcctaggtaatagaag
 P S L L A P - G S E A S G P V P R - - K
 taccatctggggctgagctctttcattttgccgtcaccaccacgaactcgctcgggtagct
 Y H L G L S S F I L P S P P R T R R V A
 cttcggtagtagccaatttgggtcatctggaccactattgggtgttgattggaacgcctgg
 L R - - P I W S S G P L L V L I G T P W
 cctcgagggaatctaagttcctccttgccatgctgagtgaagctgtgaaccaagacga
 P R G N L S S S L P C - V R A V N Q D A
 atattattgggtaaacccttggggtcggcgctgttttggccttgccccattgcagtcctcc
 I L L G K P W G R R C F G L A P L Q S S
 attctggttattgtcagttgaatctgtgggtccaccaaataatgcggggggcactacg
 I L V I V S - I C G S T K C N A G G T T
 ttggtttgattgggggtccattatcagacattttaatttgttcgtttagagaacagatcta
 L V - L G S I I R H F N L F V - R T D L
 caagagatcgaggttggttggtctttcctgggtaggtaaaaaccta
 Q E I E V G W L F L G R - K P

3'5' Frame 2

aggc aaattgtgcaatttgcggcccaatgtttgtaatcagttccttgtctgattaggtctt
 G K L C N L R P N V C N Q F L V - L G L
 ggtccccgaaatttcccttgggtttgttctggaccacgtctcccaaatagttgagtgaagt
 G P R N F L G F V L D H V S Q M L E - R
 tgtactgttttgtggcagtagcgttttggcgaggcttttttagatgcctcagcagcagatt
 C T V L W Q Y V F G E A F - M P Q Q Q I
 tcttagtgacagtttggccttgttgttgttggcctttaccagaaactttgtctcaagct
 S - - Q F G L V V V G L Y Q K L C S Q A
 ggttcaatctgtctagcagcaatagcgcgagggttccaccacctccgctagccattc
 G S I C L A A I A R G Q F H H L R - P F
 gagcaggagaatttcccctactgctgccaggagttgaatttcttgaattaccgcgactac
 E Q E N F P Y C C Q E L N F L N Y R D Y
 gtgatgaggagcgagaagaggcttgactgccgcctctgcttccctctgcgtagaagcctt
 V M R S E K R L D C R L C F P L R R S L
 ttggcaatgttgttccttgaggaagttgtagcacggtggcagcattgttattaggattgc
 L A M L F L E E V V A R W Q H C Y - D C
 ggggtgccaatgtggtctttgggtgtattcaaggctccctcagttgcaaccatacga
 G C Q C G L W V Y S R L P Q L Q P I R C
 cttctttgttagcgccgtagggaagtgaagcttctgggccagttcctaggtaatagaagt

196/199

L L C - R R R E V K L L G Q F L G N R S
 accatctggggctgagctctttcattttgccgtcaccaccacgaactcgctcgggtagctc
 T I W G - A L S F C R H H H E L V G - L
 ttcggtagtagccaatttggtcatctggaccactattgggtgttgattggaacgccctggc
 F G S S Q F G H L D H Y W C - L E R P G
 ctcgagggaatctaagttcctccttgccatgctgagtgagagctgtgaaccaagacgcaa
 L E G I - V P P C H A E - E L - T K T Q
 tattattgggtaaaccttggggtcggcgctgttttggccttgccccattgcagtcctcca
 Y Y W V N L G V G A V L A L P H C S P P
 ttctggttattgtcagttgaatctgtgggtccaccaaataatgcggggggcactacgt
 F W L L S V E S V G P P N V M R G A L R
 tggtttgattggggccattatcagacattttaatttggttcgtttagagaacagatctac
 W F D W G P L S D I L I C S F R E Q I Y
 aagagatcgagggttggttggtctttcctgggtaggtaaaaaccta
 K R S R L V G F S W V G K N L

3'5' Frame 3

aggcaaattgtgcaatttgcggcccaatgtttgtaatcagttccttgtctgattaggtcttg
 A N C A I C G P M F V I S S L S D - V L
 gtccccgaaatttcccttgggtttgttctggaccacgtctcccaaatagttgagtgacgtt
 V P E I S L G L F W T T S P K C L S D V
 gtactgttttgtggcagtagctttttggcgaggcttttttagatgcctcagcagcagattt
 V L F C G S T F L A R L F R C L S S R F
 cttagtgcaggtttggccttgttgttgttggcctttaccagaaactttgctctcaagctg
 L S D S L A L L L L A F T R N F A L K L
 gttcaatctgtctagcagcaatagcgcgagggtcagtttcaccacctccgctagccattcg
 V Q S V - Q Q - R E G S F T T S A S H S
 agcaggagaatttcccctactgctgccaggagttgaatttcttgaattaccgcgactacg
 S R R I S P T A A R S - I S - I T A T T
 tgatgaggagcgagaagaggcttgactgccgcctctgcttccctctgcgtagaagccttt
 - - G A R R G L T A A S A S L C V E A F
 tggcaatgttggtccttgaggaagttgtagcacggtggcagcattgttattaggattgcg
 W Q C C S L R K L - H G G S I V I R I A
 ggtgccaatgtggtctttgggtgtattcaaggtccctcagttgcaaccatacagatgcc
 G A N V V F G C I Q G S L S C N P Y D A
 ttctttgttagcgccgtagggaagtgaagcttctgggccaagttcctaggtaatagaagta
 F F V S A V G K - S F W A S S - V I E V
 ccactctggggctgagctctttcattttgccgtcaccaccacgaactcgctcgggtagctct
 P S G A E L F H F A V T T T N S S G S S
 tcggtagtagccaatttggtcatctggaccactattgggtgttgattggaacgccctggcc
 S V V A N L V I W T T I G V D W N A L A
 tcgagggaatctaagttcctccttgccatgctgagtgagagctgtgaaccaagacgcaat
 S R E S K F L L A M L S E S C E P R R N
 attattgggtaaaccttggggtcggcgctgttttggccttgccccattgcagtcctccat
 I I G - T L G S A L F W P C P I A V L H
 tctggttattgtcagttgaatctgtgggtccaccaaataatgcggggggcactacgtt

197/199

S G Y C Q L N L W V H Q M - C G G H Y V
ggtttgattggggtccattatcagacattttaatttgttcgtttagagaaacagatctaca
G L I G V H Y Q T F - F V R L E N R S T
agagatcgaggttggttggttttctgggtaggtaaaaaccta
R D R G W L A F P G - V K T

FIGURE 133

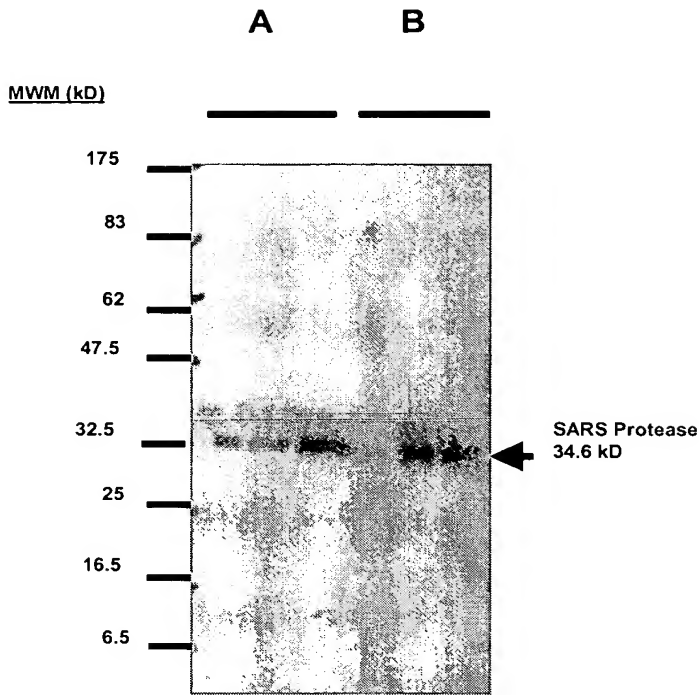


FIGURE 134

